

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 19, 2003, 07:51:03 ; Search time 237.022 Seconds

(without alignments)  
335.715 Million cell updates/sec

Title: US-09-645-835A-2  
Perfect score: 4376

Sequence: 1 VKKTYGIGSVAILLATHI.....YKNKGLVTVYDIKTLLQINP 825

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

Number of hits satisfying chosen parameters: 362588

Maximum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
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- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4166.5	95.2	793	9	US-09-252-088-15 Sequence 15, Appl
2	3769.5	86.1	715	9	US-09-252-088-16 Sequence 16, Appl
3	1054.5	24.1	838	9	US-09-884-465A-8 Sequence 8, Appl
4	1033.5	23.6	840	9	US-09-884-465A-7 Sequence 7, Appl
5	1032	23.6	763	10	US-09-765-272-66 Sequence 66, Appl
6	949	21.7	796	10	US-09-765-272-56 Sequence 56, Appl
7	920	21.0	1039	9	US-09-884-465A-6 Sequence 6, Appl
8	864	19.7	840	9	US-09-884-465A-10 Sequence 10, Appl
9	839	19.2	447	10	US-09-765-272-182 Sequence 182, Appl
10	451	10.3	1238	9	US-09-884-465A-381 Sequence 381, Appl
11	406.5	9.3	1365	9	US-09-884-465A-382 Sequence 382, Appl
12	390.5	8.9	1378	9	US-09-884-465A-378 Sequence 378, Appl
13	359.5	8.2	999	9	US-09-884-465A-377 Sequence 377, Appl
14	359	8.2	1152	9	US-09-884-465A-379 Sequence 379, Appl
15	341	7.8	1126	9	US-09-884-465A-383 Sequence 383, Appl
16	340	7.8	999	9	US-09-884-465A-376 Sequence 376, Appl
17	327	7.5	1139	9	US-09-884-465A-380 Sequence 380, Appl
18	322	7.4	94	9	US-09-884-465A-11 Sequence 11, Appl
19	269	6.1	913	9	US-09-884-465A-384 Sequence 384, Appl

20	239	5.5	906	9	US-09-884-465A-370 Sequence 370, App
21	233	5.3	900	9	US-09-884-465A-334 Sequence 334, App
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24	208	4.8	42	9	US-09-884-465A-12 Sequence 12, Appl
25	207.5	4.7	901	9	US-09-884-465A-343 Sequence 343, App
26	207	4.7	894	9	US-09-884-465A-337 Sequence 337, App
27	204	4.7	900	9	US-09-884-465A-335 Sequence 335, App
28	201.5	4.6	895	9	US-09-884-465A-347 Sequence 347, App
29	200.5	4.6	633	9	US-09-884-465A-350 Sequence 350, App
30	200.5	4.6	633	9	US-09-884-465A-354 Sequence 354, App
31	200.5	4.6	633	9	US-09-884-465A-361 Sequence 361, App
32	200.5	4.6	633	9	US-09-884-465A-362 Sequence 362, App
33	197	4.5	900	9	US-09-884-465A-339 Sequence 339, App
34	197	4.5	900	9	US-09-884-465A-341 Sequence 341, App
35	192.5	4.4	627	9	US-09-884-465A-367 Sequence 367, App
36	192	4.4	900	9	US-09-884-465A-333 Sequence 333, App
37	192	4.4	906	9	US-09-884-465A-369 Sequence 369, App
38	192	4.4	906	9	US-09-884-465A-373 Sequence 373, App
39	191.5	4.4	633	9	US-09-884-465A-351 Sequence 351, App
40	191.5	4.4	633	9	US-09-884-465A-352 Sequence 352, App
41	191.5	4.4	633	9	US-09-884-465A-357 Sequence 357, App
42	191.5	4.4	633	9	US-09-884-465A-358 Sequence 358, App
43	191.5	4.4	633	9	US-09-884-465A-359 Sequence 359, App
44	191.5	4.4	633	9	US-09-884-465A-360 Sequence 360, App
45	191.5	4.4	901	9	US-09-884-465A-345 Sequence 345, App

## ALIGNMENTS

RESULT 1  
US-09-252-088-15  
Sequence 15, Application US/09252088  
Publication No. US20030031682A1  
GENERAL INFORMATION:  
APPLICANT: BRODEUR, Bernard R.  
APPLICANT: RIOUX, Clement  
APPLICANT: BOYER, Martine  
APPLICANT: CHARLEBOIS, Isabelle  
APPLICANT: HAMEL, Jose  
APPLICANT: MARTIN, Denis  
TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS  
FILE REFERENCE: 8331-9002  
CURRENT APPLICATION NUMBER: US/09/252,088  
CURRENT FILING DATE: 1999-02-18  
EARLIER APPLICATION NUMBER: US/60/075,425  
EARLIER FILING DATE: 1998-02-20  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 15  
LENGTH: 793  
TYPE: PRT  
ORGANISM: group B streptococcus  
US-09-252-088-15

Query Match 95.2%; Score 4166.5; DB 9; Length 793;  
Best Local Similarity 98.9%; Pred. No. 3.7e-289;  
Matches 787; Conservative 4; Mismatches 2; Indels 3; Gaps 2;

QY 30 MGSATKDNQIAYIDDSKAKAPKTKNTMDQISAEEGISAEQIVKTIQDGYVTSBGDHY 89  
Db 1 MGLATKDNQIAYIDDSKAKAPKTKNTMDQISAEEGISAEQIVKTIQDGYVTSBGDHY 60  
QY 90 HFYNGKVPYDAIISELMTDPNRFKQSDVINEILDGYIVKNGNYYVYLKPGSKRKNI 149  
Db 61 HFYNGKVPYDAIISELMTDPNRFKQSDVINEILDGYIVKNGNYYVYLKPGSKRKNI 120  
QY 150 RTKQIAEQVAKGTKEAKEKGLAQAHLSTKEEYAAVNEAKRQGRYTTDDGYIFSPDIIID 209  
Db 121 RTKQIAEQVAKGTKEAKEKGLAQAHLSTKEEYAAVNEAKRQGRYTTDDGYIFSPDIIID 180  
QY 210 DLGDAYLVPFGNHVYIPKKDLSPSELAAQAQYWSQKQGRGARPSDYRPTPAPAPGRKA 269



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Db 181 DLGDAYLVPHGNHYIPEKKDLSPELAAQAQYWSQKRGARPSDYRPT--PAGRRKA 238
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Db 239 PIPDVTPNPGQGHQPDNGYHPAPRRPNDAQONKHODEFKGTEKELLDQLHRLDLKXR 298
QY 330 HVEEDGLIFEPTQVKSNAFGYVVPVPHGDHYHIIIPRSQSLPEMELADRYLAGOTEDDDSG 389
Db 299 HVEEDGLIFEPTQVKSNAFGYVVPVPHGDHYHIIIPRSQSLPEMELADRYLAGOTEDDDSG 358
QY 390 SDHSPSDKEVTHTFLGHRIRAKYKGLDGKPYDTSADAYVFSKESHSVDSKSGVTAKHGDH 449
Db 359 SEHSKPSDKSVTHTFLGHRIRAKYKGLDGKPYDTSADAYVFSKESHSVDSKSGVTAKHGDH 418
QY 450 FHYIGFGELEQYELDEVANWVAKAGQADELAALDQEQKEKPLFDTKYSRKVTAKDKGV 509
Db 419 FHYIGFGELEQYELDEVANWVAKAGQADELAALDQEQKEKPLFDTKYSRKVTAKDKGV 478
QY 510 GYMPKDKGKDYFYARDQDLTQIAFAEQELMLKDKKHRYRDIYDTGIEPRILAVDVSSLP 569
Db 479 GYMPKDKGKDYFYARDQDLTQIAFAEQELMLKDKKHRYRDIYDTGIEPRILAVDVSSLP 538
QY 570 HAGNATYDTGSSFVIPHIDHIHVVPYSWLTROQIATIKYVMOHPFVRPDIWSKPGHEESG 629
Db 539 HAGNATYDTGSSFVIPHIDHIHVVPYSWLTROQIATIKYVMOHPFVRPDIWSKPGHEESG 598
QY 630 SVIPNVTPLDKRAGMPNMQIHSAAEVOKALAEGRFATPDGYIFDPRDYLAKETFWWKD 689
Db 599 SVIPNVTPLDKRAGMPNMQIHSAAEVOKALAEGRFATPDGYIFDPRDYLAKETFWWKD 658
QY 690 SFSIPRADGSSLRITKNSDLSQAEMQAQOELLAKKNAGDATDTDKPKKQADKSNENQ 749
Db 659 SFSIPRADGSSLRITKNSDLSQAEMQAQOELLAKKNAGDATDTDKPKKQADKSNENQ 718
QY 750 PSEASKEEKESDFTDSLDPYGLDRATLEDHINQLOKANIDPKYLIQPEGVQFYNN 809
Db 719 PSEASK-EEKESDFTDSLDPYGLDRATLEDHINQLOKANIDPKYLIQPEGVQFYNN 777
QY 810 GELVITYDIKTLOQINP 825
Db 778 GELVITYDIKTLOQINP 793

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RESULT 2
US-09-252-088-16
; Sequence 16, Application US/09252088
; Publication No. US20030031682A1
GENERAL INFORMATION:
APPLICANT: BRODEUR, Bernard R.
APPLICANT: RIOUX, Clément
APPLICANT: BOYER, Martine
APPLICANT: CHARLEBOIS, Isabelle
APPLICANT: HAMEL, Jose
APPLICANT: MARTIN, Denis
TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 8331-9002
CURRENT APPLICATION NUMBER: US/09/252,088
CURRENT FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: US/60/075,425
EARLIER FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 715
TYPE: PRT
ORGANISM: group B streptococcus
US-09-252-088-16

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Query Match 86.1%; Score 3769.5; DB 9; Length 715;
Best Local Similarity 98.9%; Pred. No. 7.1e-261;
Matches 710; Conservative 4; Mismatches 1; Indels 3; Gaps 2;

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QY 108 MTDPNYREKQSDVINEILDGYVIAKNGNYYVYLKPGSKRNIRTKQOIAEOYAKGTKEAK 167
Db 1 MTDPNYREKQSDVINEILDGYVIAKNGNYYVYLKPGSKRNIRTKQOIAEOYAKGTKEAK 60
QY 168 EKGIAQVAHLSKEEVAANVEAKRQGRYTTDDGYIFSPIDIIDLDGDAYLVPHGNHYIIP 227
Db 61 EKGIAQVAHLSKEEVAANVEAKRQGRYTTDDGYIFSPIDIIDLDGDAYLVPHGNHYIIP 120
QY 228 KKDLSPELAAQAQYWSQKRGARPSDYRPTPAPAPGRKAPIPDVTPNPGQGHQPDNG 287
Db 121 KKDLSPELAAQAQYWSQKRGARPSDYRPT--PAGRRKAPIPDVTPNPGQGHQPDNG 178
QY 288 GYHPADPRPNDAQONKHODEFKGTEKELLDQLHRLDLKRYHVEEDGLIFEPTQVIRKSN 347
Db 179 GYHPADPRPNDAQONKHODEFKGTEKELLDQLHRLDLKRYHVEEDGLIFEPTQVIRKSN 238
QY 348 AFGYVVPVPHGDHYHIIIPRSQSLPEMELADRYLAGOTEDDDSGSDHSPSDKEVTHTFLGH 407
Db 239 AFGYVVPVPHGDHYHIIIPRSQSLPEMELADRYLAGOTEDDDSGSEHSKPSDKSVTHTFLGH 298
QY 408 RIKAYGKGLDGKPYDTSADAYVFSKESHSVDSKSGVTAKHGDHFIHYIGFGELEQYELDEVA 467
Db 299 RIKAYGKGLDGKPYDTSADAYVFSKESHSVDSKSGVTAKHGDHFIHYIGFGELEQYELDEVA 358
QY 468 NWVAKAGQADELAALDQEQKEKPLFDTKYSRKVTAKDKGVYMPKDKGKDYFYARDQ 527
Db 359 NWVAKAGQADELAALDQEQKEKPLFDTKYSRKVTAKDKGVYMPKDKGKDYFYARDQ 418
QY 528 DLQOIAFAEQELMLKDKKHRYRDIYDTGIEPRILAVDVSSLPMAHAGNATYDTGSSFVIPH 587
Db 419 DLQOIAFAEQELMLKDKKHRYRDIYDTGIEPRILAVDVSSLPMAHAGNATYDTGSSFVIPH 478
QY 588 DHIHVVPYSWLTROQIATIKYVMOHPFVRPDIWSKPGHEESGVIIPNVTPLDKRAGMPN 647
Db 479 DHIHVVPYSWLTROQIATIKYVMOHPFVRPDIWSKPGHEESGVIIPNVTPLDKRAGMPN 538
QY 648 QIHSAAEVOKALAEGRFATPDGYIFDPRDYLAKETFWWKDGSFISIPRADGSSLRITKNS 707
Db 539 QIHSAAEVOKALAEGRFATPDGYIFDPRDYLAKETFWWKDGSFISIPRADGSSLRITKNS 598
QY 708 DLSQAEMQAQOELLAKKNAGDATDTDKPKKQADKSNENQOPSEASK-EEKESDFTIDS 767
Db 599 DLSQAEMQAQOELLAKKNAGDATDTDKPKKQADKSNENQOPSEASK-EEKESDFTIDS 657
QY 768 LPDYGDRATLEDHINQLOKANIDPKYLIQPEGVQFYNNKNGELVITYDIKTLOQINP 825
Db 658 LPDYGDRATLEDHINQLOKANIDPKYLIQPEGVQFYNNKNGELVITYDIKTLOQINP 715

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```

RESULT 3
US-09-884-465A-8
; Sequence 8, Application US/09884465A
; Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 838
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-884-465A-8

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> 0 <  
0110 Intelligenetics  
> 0 <

FastDB: Fast Pairwise Comparison of Sequences  
Release 5.4

Results file 645835x252088.res made by msmtch on Wed 28 May 103 13:41:32-PDT.

Query sequence being compared: US-09-645-835A-7 (1-816)  
Number of sequences searched: 2  
Number of scores above cutoff: 2

Results of the initial comparison of US-09-645-835A-7 (1-816) with:  
File: US09252088mod.pep

100-  
50-  
0-  
N  
E  
R  
O  
F  
S  
U  
Q  
E  
N  
C  
E  
S  
SCORE 0 1 10 21 31 42 52 63 73 84 94  
STDEV -3 -2 -1 0 1

PARAMETERS

Similarity matrix Unitary 1 K-tuple  
Mismatch penalty 1.00 Joining penalty 2  
Gap penalty 0.05 Window size 500  
Off score 0  
Randomization group 0

SEARCH STATISTICS

Scores: Mean 79 Median 65 Standard Deviation 21.21  
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 1508  
Number of sequences searched: 2  
Number of scores above cutoff: 2

The scores below are sorted by initial score.  
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt. Score	Sig. Frame
---------------	-------------	--------	-------	------------	------------

1. US-09-252-088B-1	Sequence 15, Application	793	94	244	0.71 0
2. US-09-252-088B-1	Sequence 16, Application	715	64	193	-0.71 0

1. US-09-645-835A-7 (1-816)  
US-09-252-088B-1 Sequence 15, Application US/09252088B

Sequence 15, Application US/09252088B  
GENERAL INFORMATION:

APPLICANT: BRODEUR, Bernard R.  
APPLICANT: RIOUX, Clement  
APPLICANT: BOYER, Martine  
APPLICANT: CHARLEBOIS, Isabelle  
APPLICANT: HAMEL, Josee  
TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS  
FILE REFERENCE: 8331-9002  
CURRENT APPLICATION NUMBER: US/09/252, 088B  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US/60/075, 425  
PRIOR FILING DATE: 1998-02-20  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 15  
LENGTH: 793  
TYPE: PRT  
ORGANISM: group B streptococcus

Initial Score = 94 Optimized score = 244 Significance = 0.71  
Residue Identity = 34% Matches = 295 Mismatches = 423  
Gaps = 149 Conservative Substitutions = 0

MKINKKYLVGSAALLILSVCSYELGLQARTVKENRVSYID--GKQATOKTENTLPDEVSKEGINAEQI  
MGL-----ATKDN-QIAYIDSKGAKAPKT-NKIMDOIASEGISAEQI  
X 10 20 30 40 50 60 70 80 90 100 110 120 130 140

VIKITDQGYTSHGDHYHYNGKVPYDAIIESELMKDPNPKLDEDIVNEVKGYYRVKDGKYYVEKDA  
VVKITDQGYTSHGDHYHYNGKVPYDAIIESELMKDPNPKLDEDIVNEVKGYYRVKDGKYYVEKDA  
50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200

HADNVRTKEEINRO--KQHSQHREG-----GTPRNDGAVALLARSQGRYTTDDGYIFNASDIETGDAI  
KRKNIRTKQQLACQVAKGTKEAKEKGLAQAVALSKKEEVAANAEAKRQGRYTTDDGYIFNASDIETGDAI  
120 130 140 150 160 170 180 190 200 210 220 230 240 250 260

VPHGDIHYTPKNELASASELAAPLS---GRG-NLSNSR---TYRR--QNSDNTSRTNWVPSVSNPQGT  
VPHGNHYHYTPKNDLSPSELAAQAYWSQKGRGARPSPDIPTAPGRKAPIPDVTPNPGQHDPDNG--  
190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340

NTNTSNNSTNSQASQSDN-----IDSELKOLYKLPQSRYVESDGLVFDPAQITSTRARGAVPHGDHYH  
YHPAPPRPNDASQNHORDEFKGTKEKELIDOLHRLDKRYHVEEDGLIFPTQVKSNAFGYVPHGDHYH  
260 270 280 290 300 310 320 330 340 350 360 370 380 390 400

FIPYSQMSLEERLARIPLRYRSHNWVPSRPEQSPQPTPEPSGPQAPAPNLKIDSNSLSVQLVRKVG  
IIPRSQLSPELELA---DRY-----LAGQTEDNDGSGEHSKPSDKVYHTFL-GHRIKAYGK  
330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480

GVVFEKGIS-RYVFAKDLPSFYVKNLESKLSKQESVSHLTAKENVAPRDQEFYDKAYNLLTEA--HKAL







GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 19, 2003, 07:51:03 ; Search time 237.022 Seconds

(without alignments)  
335.715 Million cell updates/sec

Title: US-09-645-835A-2

Perfect score: 4376

Sequence: 1 VKKTYGYIGSVAILLATHI.....YKNKGELVTYDIKTLQINP 825

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

Total number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
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6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
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12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3769.5	86.1	715	9	US-09-252-088-16 Sequence 16, Appl
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8	864	19.7	840	9	US-09-884-465A-10 Sequence 10, Appl
9	839	19.2	447	10	US-09-765-272-182 Sequence 182, Appl
10	451	10.3	1238	9	US-09-884-465A-381 Sequence 381, Appl
11	406.5	9.3	1365	9	US-09-884-465A-382 Sequence 382, Appl
12	390.5	8.9	1378	9	US-09-884-465A-378 Sequence 378, Appl
13	359.5	8.2	999	9	US-09-884-465A-377 Sequence 377, Appl
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15	341	7.8	1126	9	US-09-884-465A-383 Sequence 383, Appl
16	340	7.8	999	9	US-09-884-465A-376 Sequence 376, Appl
17	327	7.5	1139	9	US-09-884-465A-380 Sequence 380, Appl
18	322	7.4	94	9	US-09-884-465A-11 Sequence 11, Appl
19	269	6.1	913	9	US-09-884-465A-384 Sequence 384, Appl

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21	233	5.3	900	9	US-09-884-465A-334	Sequence 334, App
22	230	5.3	906	9	US-09-884-465A-332	Sequence 332, App
23	220	5.0	906	9	US-09-884-465A-372	Sequence 372, App
24	208	4.8	42	9	US-09-884-465A-12	Sequence 12, Appl
25	207.5	4.7	901	9	US-09-884-465A-343	Sequence 343, App
26	207	4.7	904	9	US-09-884-465A-337	Sequence 337, App
27	204	4.7	900	9	US-09-884-465A-335	Sequence 335, App
28	201.5	4.6	895	9	US-09-884-465A-347	Sequence 347, App
29	200.5	4.6	633	9	US-09-884-465A-350	Sequence 350, App
30	200.5	4.6	633	9	US-09-884-465A-354	Sequence 354, App
31	200.5	4.6	633	9	US-09-884-465A-361	Sequence 361, App
32	200.5	4.6	633	9	US-09-884-465A-362	Sequence 362, App
33	197	4.5	900	9	US-09-884-465A-339	Sequence 339, App
34	197	4.5	900	9	US-09-884-465A-341	Sequence 341, App
35	192.5	4.4	627	9	US-09-884-465A-367	Sequence 367, App
36	192	4.4	900	9	US-09-884-465A-333	Sequence 333, App
37	192	4.4	906	9	US-09-884-465A-369	Sequence 369, App
38	192	4.4	906	9	US-09-884-465A-373	Sequence 373, App
39	191.5	4.4	633	9	US-09-884-465A-351	Sequence 351, App
40	191.5	4.4	633	9	US-09-884-465A-352	Sequence 352, App
41	191.5	4.4	633	9	US-09-884-465A-357	Sequence 357, App
42	191.5	4.4	633	9	US-09-884-465A-358	Sequence 358, App
43	191.5	4.4	633	9	US-09-884-465A-359	Sequence 359, App
44	191.5	4.4	633	9	US-09-884-465A-360	Sequence 360, App
45	191.5	4.4	901	9	US-09-884-465A-345	Sequence 345, App

ALIGNMENTS

RESULT 1  
US-09-252-088-15  
; Sequence 15, Application US/09252088  
; Publication No. US20030031682A1  
; GENERAL INFORMATION:  
; APPLICANT: BRODEUR, Bernard R.  
; APPLICANT: RIOUX, Clment  
; APPLICANT: BOYER, Martine  
; APPLICANT: CHARLEBOIS, Isabelle  
; APPLICANT: HAMEL, Jose  
; APPLICANT: MARTIN, Denis  
; TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS  
; FILE REFERENCE: 8331-9002  
; CURRENT APPLICATION NUMBER: US/09/252,088  
; CURRENT FILING DATE: 1999-02-18  
; EARLIER APPLICATION NUMBER: US/60/075,425  
; EARLIER FILING DATE: 1998-02-20  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 793  
; TYPE: PRT  
; ORGANISM: group B streptococcus  
US-09-252-088-15

Query Match 95.2%; Score 4166.5; DB 9; Length 793;  
Best Local Similarity 98.9%; Pred. No. 3.7e-289;  
Matches 787; Conservative 4; Mismatches 2; Indels 3; Gaps 2;

QY 30 MGSATKDNQAIYIDDSKGKAKAPKTKNTMDQISAEGISAEQIVYKTTDQGYVTSBGDHY 89  
Db 1 MGLATKDNQAIYIDDSKGKAKAPKTKNTMDQISAEGISAEQIVYKTTDQGYVTSBGDHY 60  
QY 90 HFYNGKVPYDAIISELLMTDPNRYRKQSDVINEIILDGYVIKYNNGNYYVYLKPGSKRRNI 149  
Db 61 HFYNGKVPYDAIISELLMTDPNRYRKQSDVINEIILDGYVIKYNNGNYYVYLKPGSKRRNI 120  
QY 150 RTKQIAEQVAKGTKEAKEKGLAQVAHLSKEEVAAVNEAKRQGRYTTDDGYIFSPDTIID 209  
Db 121 RTKQIAEQVAKGTKEAKEKGLAQVAHLSKEEVAAVNEAKRQGRYTTDDGYIFSPDTIID 180  
QY 210 DLGDAYLVPHGNHYHYIPKKDLSPSELAQAAYWSQKQGRGARPSDYRPTPAPAGRRKA 269

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|||||
Db 181 DLGDAYLVPHGNHYHYPKDDLSPSELAAQAAYWSQKQGRGARPSPDYRPT--PAPGRKKA 238

QY 270 PIPDVTNPNQGHQPDNGGYHPAPRPNDASQNKHQRDEFEKGTKEKELLDQLHRLDLKYR 329
|||||
Db 239 PIPDVTNPNQGHQPDNGGYHPAPRPNDASQNKHQRDEFEKGTKEKELLDQLHRLDLKYR 298

QY 330 HVEEDGLFEPTQVIXSNAFGYVVPBGDHYHIIPRSQLSPLEMELADRYLAGQTEDDSDG 389
|||||
Db 299 HVEEDGLFEPTQVIXSNAFGYVVPBGDHYHIIPRSQLSPLEMELADRYLAGQTEDDSDG 358

QY 390 SDHSKPSDKEVHTFLGHRIRKAYGKGLDGKPYDTSDAYVFSKESHSVDSKSGVTAKHGDH 449
|||||
Db 359 SEHSKPSDKEVHTFLGHRIRKAYGKGLDGKPYDTSDAYVFSKESHSVDSKSGVTAKHGDH 418

QY 450 FHYIGFGELEQYELDEVANWVKAKGQADELAALDQEQKEKPLFDTKKVSRRKVTKDGY 509
|||||
Db 419 FHYIGFGELEQYELDEVANWVKAKGQADELAALDQEQKEKPLFDTKKVSRRKVTKDGY 478

QY 510 GYMPKDGKDYFYARDQLDLTQIAFAEQELMLKDKKHRYDYVDTGIEPRLAVDVSSLPM 569
|||||
Db 479 GYMPKDGKDYFYARDQLDLTQIAFAEQELMLKDKKHRYDYVDTGIEPRLAVDVSSLPM 538

QY 570 HAGNATYDTGSSFVIPHIDHIVVPYSWLTQDIATIKYVMQHPVPRDIMSCKPGHEESG 629
|||||
Db 539 HAGNATYDTGSSFVIPHIDHIVVPYSWLTQDIATIKYVMQHPVPRDIMSCKPGHEESG 598

QY 630 SVIPNVTPLDKRAGMPNWOIHSAAEVOKALAEGRFATPDGYIFDPRDYLAKETFWWKDG 689
|||||
Db 599 SVIPNVTPLDKRAGMPNWOIHSAAEVOKALAEGRFATPDGYIFDPRDYLAKETFWWKDG 658

QY 690 SFSIPRADGSSLRTINKSDLSQAEMQOQELLAKKNAGDATDTDKPEKQOADSNNQO 749
|||||
Db 659 SFSIPRADGSSLRTINKSDLSQAEMQOQELLAKKNAGDATDTDKPEKQOADSNNQO 718

QY 750 PSEASKESKESDDFIDSLPDYGLDRATLEHDHINQLAOKANIDPKYLIQPEGVQFYNNK 809
|||||
Db 719 PSEASK-EEKESDDFIDSLPDYGLDRATLEHDHINQLAOKANIDPKYLIQPEGVQFYNNK 777

QY 810 GELVTYDIKTLOQINP 825
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Db 778 GELVTYDIKTLOQINP 793
```

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RESULT 2
US-09-252-088-16
; Sequence 16, Application US/09252088
; Publication No. US20030031682A1
; GENERAL INFORMATION:
; APPLICANT: BRODEUR, Bernard R.
; APPLICANT: RIOUX, Clément
; APPLICANT: BOYER, Martine
; APPLICANT: CHARLEBOIS, Isabelle
; APPLICANT: HAMEL, Jose
; APPLICANT: MARTIN, Denis
; TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS
; FILE REFERENCE: 8331-9002
; CURRENT APPLICATION NUMBER: US/09/252,088
; CURRENT FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: US/60/075,425
; EARLIER FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 715
; TYPE: PRT
; ORGANISM: group B streptococcus
US-09-252-088-16
```

Query Match 86.1%; Score 3769.5; DB 9; Length 715;  
Best Local Similarity 98.9%; Pred. No. 7.1e-261;  
Matches 710; Conservative 4; Mismatches 1; Indels 3; Gaps 2;

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QY 108 MTDPNYRFKQSDVINEILDGYIVKNGNYVYLKPGSKRNIRTKQOIAEQVAKGTKEAK 167
|||||
Db 1 MTDPNYRFKQSDVINEILDGYIVKNGNYVYLKPGSKRNIRTKQOIAEQVAKGTKEAK 60

QY 168 EKGLAQAHLKSKEVAAVNEAKRQGRYTTDDGYIESPTDIIDDLGAYLVPHGNHYHYP 227
|||||
Db 61 EKGLAQAHLKSKEVAAVNEAKRQGRYTTDDGYIESPTDIIDDLGAYLVPHGNHYHYP 120

QY 228 KKDLSPELAAAQAAYWSQKQGRGARPSPDYRPTAPAPGRKAPIPDVTNPNQGHQPDNG 287
|||||
Db 121 KKDLSPELAAAQAAYWSQKQGRGARPSPDYRPT--PAPGRKAPIPDVTNPNQGHQPDNG 178

QY 288 GYHPAPRPNDASQNKHQRDEFEKGTKEKELLDQLHRLDLKYRHVEEDGLFEPTQVIXSN 347
|||||
Db 179 GYHPAPRPNDASQNKHQRDEFEKGTKEKELLDQLHRLDLKYRHVEEDGLFEPTQVIXSN 238

QY 348 AFGYVVPBGDHYHIIPRSQLSPLEMELADRYLAGQTEDDSDGSDHSKPSDKEVHTFLGH 407
|||||
Db 239 AFGYVVPBGDHYHIIPRSQLSPLEMELADRYLAGQTEDDSDGSEHSKPSDKEVHTFLGH 298

QY 408 RIKAYGKGLDGKPYDTSDAYVFSKESHSVDSKSGVTAKHGDHFIYIGFGELEQYELDEVA 467
|||||
Db 299 RIKAYGKGLDGKPYDTSDAYVFSKESHSVDSKSGVTAKHGDHFIYIGFGELEQYELDEVA 358

QY 468 NWWKAKGQADELAALDQEQKEKPLFDTKKVSRRKVTKDGYVGYMPKDGKDYFYARDQL 527
|||||
Db 359 NWWKAKGQADELAALDQEQKEKPLFDTKKVSRRKVTKDGYVGYMPKDGKDYFYARDQL 418

QY 528 DLQIAFAEQELMLKDKKHRYDYVDTGIEPRLAVDVSSLPMHAGNATYDTGSSFVIPH 587
|||||
Db 419 DLQIAFAEQELMLKDKKHRYDYVDTGIEPRLAVDVSSLPMHAGNATYDTGSSFVIPH 478

QY 588 DHIHVVPYSWLTQDIATIKYVMQHPVPRDIMSCKPGHEESGSVIPNVTPLDKRAGMPN 647
|||||
Db 479 DHIHVVPYSWLTQDIATIKYVMQHPVPRDIMSCKPGHEESGSVIPNVTPLDKRAGMPN 538

QY 648 QITHSAEEVOKALAEGRFATPDGYIFDPRDYLAKETFWWKDGSFIPRADGSSLRTINKS 707
|||||
Db 539 QITHSAEEVOKALAEGRFATPDGYIFDPRDYLAKETFWWKDGSFIPRADGSSLRTINKS 598

QY 708 DLSQAEMQOQELLAKKNAGDATDTDKPEKQOADSNNQOPEASEKESKESDDFIDS 767
|||||
Db 599 DLSQAEMQOQELLAKKNAGDATDTDKPEKQOADSNNQOPEASEK-EEKESDDFIDS 657

QY 768 LPDYGLDRATLEHDHINQLAOKANIDPKYLIQPEGVQFYNNKNGELVTYDIKTLOQINP 825
|||||
Db 658 LPDYGLDRATLEHDHINQLAOKANIDPKYLIQPEGVQFYNNKNGELVTYDIKTLOQINP 715
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```
RESULT 3
US-09-884-465A-8
; Sequence 8, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 838
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-884-465A-8
```



Query Match	24.18;	Score 1054.5;	DB 9;	Length 838;
Best Local Similarity	35.68;	Pred. No. 6.5e-67;		
Matches 279;	Conservative 101;	Mismatches 235;	Indels 169;	Gaps 31;
QY 1 VKTGYIGSVAAIILATHIGSYOLGHHMGSATKD-NQIAYIDDSKGAAPKTNKTMD	59			
Db 3 INKRY-LAGSVA--VLALSVCSEYELGRHQAGQVKKESNRVSIIDGDQAGOKA--ENLTPD	57			
QY 60 QISAEEGISAEQIVKKTDDGYVTSBGDHYHFYNGKVPYDAITISELLMTDPNRYFKQSD	119			
Db 58 EVSKREGINAEQIVIKITDDGYVTSBGDHYHYNGKVPYDAITISELLMKDPNYQLKSD	117			
QY 120 VINEILDGYIVIKVNGNYYVYLKPGSKRKNIIRTKQIAEQVAKGTKEAKEKGLAQVAHLK	179			
Db 118 IVNEIKGGYIVIKVDGKYVYVLKDAHADNIRTKKEIKRKQKEHSHN-----HNSR	167			
QY 180 EEVAAVNEAKRQGRYTTDDGYTFSPDTIIDDLGDAYLVPHGNHYIIPKDLSPSELAAA	239			
Db 168 AD-NAVAARAQGRYTTDDGYTFNASDIIEDTDAYIVPHGDHYHYIPKNELASSELAAA	226			
QY 240 QATWSOKQG-RGARPSDYRPTAPAPGRKKAPIPDVTNPGQGHQ---PDNGYHPAP	294			
Db 227 EAYWNGKQGSRPSSSSSYNANP-----VQPRLESHNLLTVPT--YH----	266			
QY 295 RPNDAQONKHQRDEFKGTKEKLLDQLHRLDLKYRHVEEDGLIEPTQVIXSNAFGYVP	354			
Db 267 -----QN-----QGENISSLLRELAKPLSERHVESDGLTFDAQITSRTARGVAVP	313			
QY 355 HGDHYHIIPRSQLSPEMELAD---RYLAGQTEDDSDGSDHSKPSDKEVTHFLGHRK	410			
Db 314 HGNHYHFIPYEQMSELEKRLAIRILRYRSNHWVPD--SRDEQSPQSTPEPSPSLQPA	370			
QY 411 AYGKGLDGKPYDTSDAYVFSKESIHSDVDSGVTAKHGDHFFHYIGFGELEQYELDEVANWV	470			
Db 371 PNPQAPAPSNPIDEK---LVKEAVRV-----GDGY-----VFEENGVSRYI	408			
QY 471 KAKGQADELAAALDQEQCKEPLFDTKKVSRKVTKDGKGYTMMPKDGKDYFYARDQLLT	530			
Db 409 PAKDLSAETAAGIDSKLAKQESL--SHKLGAKKTD-----LPSSDREFY--NKAYDL-	456			
QY 531 QIAFAEQELMLKDKKHRYRDIIVDTGIEPRLAVDVSSLPMHAGNATYDTGSSFVIPHIDHI	590			
Db 457 -LARIHQDLLDNKGROYDFEVLNMLE-RLK-DVSS-----DKV 492				
QY 591 HVPVYSWLTRODIATIKYVMOHPEVRPDIWSKPGHEESGVIINVTPLDKRAGMPNWQII	650			
Db 493 KLV-----DILAFAPIRHPE-----RLGKPNQGIT 519				
QY 651 HSAEEVQKALAEGRFATPDGYTFDPRLVLAKETFWKDGFSIPRADGSSLRTINKSDLS	710			
Db 520 YTDEIQAQVAKLAGKYTTEDGYTFDPRDITSE-----GDAYVTPMTHS--HWIKDSLS	572			
QY 711 QAEMQQAQELLAKKNAGDATDTDKPKKEQQAADKSNENOQPSAEKKEEKESDDE-IDSLP	769			
Db 573 EAERAAQAQYAKERCL-----TPPSTDHQDSGNTAEKGAFAIYNRVKAARKVPLDRMP	625			
QY 770 DYGL 773				
Db 626 -YNL 628				
RESULT 4				
US-09-884-465A-7				
Sequence 7, Application US/09884465A				
Publication NO. US20030077293A1				
GENERAL INFORMATION:				
APPLICANT: Shire Biochem, Inc.				
APPLICANT: Hamel, Josee				
APPLICANT: Brodeur, Bernard				
APPLICANT: Martin, Denis				
APPLICANT: Charland, Nathalie				
APPLICANT: Ouellet, Catherine				

[illegible]





TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 796 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 56:  
US-09-765-272-56

Query Match 21.7%; Score 949; DB 10; Length 796;  
Best local Similarity 29.5%; Pred. No. 2.1e-59;  
Matches 277; Conservative 100; Mismatches 214; Indels 348; Gaps 34;

QY 22 SYQLGKHHMGSA TKDNQIAYIDSKGAKAPKT-NKIMDOISAEGISAEQIVKTI TDG 80  
DB 1 SYELGLYQARTVKENNRVSID--GKQATQKTENTLPDEVSKREGINAEQIVIKITDQG 57  
QY 81 YVTSHGDIHYFYNGKVPYDAIISELLMTDPNRFKQSDVINEILDGYVIVKNGNYVYL 140  
DB 58 YVTSHGDIHYFYNGKVPYDAIISELLMKDPNFKLDEDIYNEVGKGYIVKVDGKRYVYL 117  
QY 141 KPGSKRNKIRTKQOIAEQVAKGTKEAKEKGLAQAHAHLSKEEVAAVNEAKRQGRYTTDDGY 200  
DB 118 KDAHADNVRTKEEINRQKEHQH-REGG-----TPRNDGAVALARSQGRYTTDDGY 169  
QY 201 IFSPTDIIDLDGDAYLVPHGNHYIIPKDLSPSELAAQAYWSOKQGRG--ARPSDYRP 258  
DB 170 IFNASDIETDGDAYIVPHGDHYIIPKNELASASELAAEAFLS--GRGNLSNRYRR 226  
QY 259 TPAPAGRRKAPIPDVTNPGQGHQPDNGGYHPAPRPNDASQNKHQRDEFEKGTFFKELL 318  
DB 227 QNSDNTSRTNW-VPSVS-NPGTTNTNTSN-----NSNTNSQASQSDN-----IDSL 271  
QY 319 DQLRLDLKYRHAEEEDGLIFEPTQVYIKSNAFGYVPHGDHYIIPRSQLSPLEMEIAD-- 376  
DB 272 KQLYKLPQSQRHVESDGLVFDAQITSRTARGVAVPHGDHYHPIYQSOMSELEERTARI 331  
QY 377 --RYLAGQTEDD-----DSGSD----- 391  
DB 332 PLRYRSNHWVPDSRPEQSPQTPERPSPQAPAPNLKIDSNSSLVSQLVKRVGEGYFEE 391  
QY 392 -----HSKRPSDKE-VTHTFLGHR-----IKAY----- 412  
DB 392 KGISRYVFAKDLPSSETVKNLESKLSQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAH 451  
QY 413 -----GKGLD-----GKP----- 420  
DB 452 KALEYXNKGKNSDFQALDKLERLNDESTNKEKLVDDLAFAPITHPERLKGKPNQIEYT 511  
QY 421 -----YDTSDAVYFSKESHSVDKSGVTAKHGDHFHYIGFGELEQYELDEVAN 468  
DB 512 EDEVYRIQLADKYTTSQGYLFEDEHDIISDEGDAYVTPHMGSHWIGKDSLSDKERYAAQA 571  
QY 469 WVKAKG-----QADELAALDOEQKEK-PLFDTKKVSRKVTGDKGYGMM 513  
DB 572 YTKERGLPPSPDADVKANPTGDSAAAIYNRVKGKGRIFLV-----RLPYMV 618  
QY 514 PKDGKDYFYARDQLDTQIAFAEQELMLKDKKHRYVDIVDTGIEPRLAVDVSSLEPMHAGN 573  
DB 619 -----EH-----TVEVKN-----GN 628  
QY 574 ATYDTGSSFVIPHIDHIVVYSWL-----TRDQIATIKYVMQHPEVRP--D 618  
DB 629 -----LIPHKDHYHNKIFAWFDDHTYKAPNGYTLLEDLFATIKYVEHDERPHSND 680  
QY 619 IWSKPGHEESGVIPIVNTPLDKRAGMPNWOIHSAEVYQKALAEGRFATPDGYTFDPRDY 678  
DB 681 GW-----GNASEHYLGKDKHSEDPNKNFKADEEPEVEETPAE-----PE----- 718

QY 679 LAKETFWKDGSPSIPRADGSSLRITINKSDISQAEMQAOELLAKN---AGDATDT-- 732  
DB 719 -----VPQVE-----TEKVEAQKAEVLLAKYTDSSLKANATETLLA 755  
QY 733 -----DKPEKQQADK--SNENOQPSSEASKEE 757  
DB 756 GLRNNLTLQIMDNNSIMAEKLLALLKGSNPSSVSKEK 794

RESULT 7  
US-09-884-465A-6  
; Sequence 6, Application US/09884465A  
; Publication No. US20030077293A1  
; GENERAL INFORMATION:  
; APPLICANT: Shire Biochem, Inc.  
; APPLICANT: Hamel, Josee  
; APPLICANT: Brodeur, Bernard  
; APPLICANT: Martin, Denis  
; APPLICANT: Charland, Nathalie  
; APPLICANT: Ouellet, Catherine  
; TITLE OF INVENTION: Streptococcus Antigens  
; FILE REFERENCE: 055190-0044  
; CURRENT APPLICATION NUMBER: US/09/884,465A  
; CURRENT FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: 60/212,683  
; PRIOR FILING DATE: 2000-06-20  
; NUMBER OF SEQ ID NOS: 384  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 1039  
; TYPE: PR  
; ORGANISM: Streptococcus pneumoniae  
US-09-884-465A-6

Query Match 21.0%; Score 920; DB 9; Length 1039;  
Best local Similarity 26.5%; Pred. No. 3.6e-57;  
Matches 262; Conservative 158; Mismatches 298; Indels 270; Gaps 31;

QY 7 YIGSVAAILLATHIGSYQLGKHHMGSA TKDNQIAYIDSKGAKAPKTNTMDOISAEEG 66  
DB 7 YIAGSAVIVSLSCAYALNQHRSQENKDNRRVSYVDGSQSQKS--ENLTPDQVSQKEG 64  
QY 67 ISAEQIVKIIDQGYVTSHGDIHYFYNGKVPYDAIISELLMTDPNRYFKQSDVINEILD 126  
DB 65 IQAEQIVIKITDQGYVTSHGDIHYFYNGKVPYDALFSELLMKDPNYQLKADIVNEVKG 124  
QY 127 GYVIVKNGNYVYVLPKPGSKRNKIRTKQOIAEQVAKGTKEAKEKGLAQAHAHLSKEEVAAVN 186  
DB 125 GYIIVKDGKYYVYLKDAHADNVRTKDELNRQKEHVKD-NEKVNNSVA----- 172  
QY 187 EAKRQGRYTTDDGYIFSPTDIIDLDGDAYLVPHGNHYIIPKDLSPSELAAQAYWSOK 246  
DB 173 VARSQGRYTTNDGYVFNPAIDIEDTGNAIVPHGDHYIIPKDLASASELAAKAHLA-- 230  
QY 247 QGRGARPSDYRTPAPAPGRKAPIPDVTNPGQGHQPDNGGYHPAPRPNDASQNKHOR 306  
DB 231 -GKNMQPSQLSYSTASDNNTQSVAKGSTSKPAN----- 263  
QY 307 DEFKGTFFKELLQDLRLDKYRHAEEEDGLIFEPTQVYIKSNAFGYVPHGDHYIIPRSQ 366  
DB 264 --KSENLOSLKELLYDSPAQRYSQGLVFDPAKTIISRTPNVAIPHGDHYHFIYPSK 320  
QY 367 LSPLEMEIADRYL---AGQTEDDS-----GSDHSPS-----DKEVTHFLGHR 409  
DB 321 LSALEEKIA-RMVPISGTGSTVSTNAKNEVSSISGLSSNPSSLTTSKELS----- 371  
QY 410 KAYGKGLDGKPYDTSDAYVFSKESHSVDKSGVTAKHGDHFHYI-GFGELEQYELDEVAN 468  
DB 372 -----SASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPN--N 417  
QY 469 WVKAKGQADELAALDOEQKEKPL-FDTKKVSRKVTGDKGYGMMPKDGKDYFYARDQL 527  
DB 418 SLATPSPSLPINGTSHKHEEDGYGFD-----ANRIIAEDESGLFVMSHGDNHNYFFKKDL 473

QY	528	DLTQIAFAEQELMLKOKKHRYDI-----VDTGIEPRLAVDYSSLLPMH	570
Dd	474	TEEOIKAAOQHLEEVKTSHNGLDLSHSHEQDYPGNAKEMKDLDKKIIEEKIAGIMKOYGVK	533
QY	571	AGNATYDTGSGSFEVI-PHIDHIHVVPYSWLTRDOIATI-----KYVMQHPEVRPDIWSK	622
Dd	534	RESIVVNKEKNMAIIYPHGDDHHADPI-----DEHKPVGIGHSHSNYELEFKPE--EGVAKK	586
QY	623	PGHE-ESGSVIPNTVPLDKRAGMPMWOI-----IHSAEEVOKALAEGB--REATP	668
Dd	587	EGNKVYTGEELTNVVNLKLNSTFNNOQFTLANGOKRVSFSPPELEKKLGINMLVKLITP	646
QY	669	DGYIFD-----PRDVLAKETF-----WMDGSFSIPRA--	696
Dd	647	DGKVLKESGVKGVEGCVGNIANFELDQPYLLPGQTFKYTTIASKNDYPEVSXDGTFIVPTSLA	706
QY	697	-----	696
Dd	707	YKMASOTIFYPFHAGDTYLRLVNPQFAVPKGTDALVRVFDEFHCNAYLENMYKVGEIKLP I	766
QY	697	----DSSSLRTINKSDL-----SOAEWQAQELLAKKNGDATDTPK-----	735
Dd	767	PKLNOGTTTRTAGNKIPVTFMANAYILDNOSTYIVEVPILEKEN-----QTDPKSILPOFKR	821
QY	736	KEKQAADKSNEHQPSSEASKEEKE-----SDDFIDSLEDYGLDRATLEDHINO LA	786
Dd	822	NKAQENSKLDEKVEEPKTSSEKVEKEKSETGNSTNSSTLEEVPTVD---PVQEKVAKFA	877
QY	787	QKANIDPKYLIFOPEG-VQFYNNKNGELV	813
Dd	878	ESYGMKLENVLFNMDSGTIELYLLPSGEVI	905

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RESULT 8
US-09-884-465A-10
; Sequence 10, Application US/09884465A
; Publication No. US20030077293A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Shire Biochem, Inc.
;
; APPLICANT: Hamel, Josee
;
; APPLICANT: Brodeur, Bernard
;
; APPLICANT: Martin, Denis
;
; APPLICANT: Charland, Nathalie
;
; APPLICANT: Ouellet, Catherine
;
; TITLE OF INVENTION: streptococcus Antigens
;
; FILE REFERENCE: 055190-0044
;
; CURRENT APPLICATION NUMBER: US/09/884,465A
;
; CURRENT FILING DATE: 2001-06-20
;
; PRIOR APPLICATION NUMBER: 60/212,683
;
; PRIOR FILING DATE: 2000-06-20
;
; NUMBER OF SEQ ID NOS: 384
;
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 10
;
; LENGTH: 840
;
; TYPE: PRT
;
; ORGANISM: Streptococcus pneumoniae
US-09-884-465A-10

```

Query Match	19.7%;	Score 864;	DB 9;	Length 840;
Best Local Similarity	28.4%;	Pred. No. 2.6e-53;		
Matches 267; Conservative	144;	Mismatches 273;	Indels 256;	Gaps 43;

[illegible]

Dh	120	DAAHADNVRIKDEINRQKQEHVKD--NEKVN\$NVA-----	VAR\$QGRYTTNDGYV	167
QY	202	FSPTDIIDDIGDAYLVPHGNHYH1PKKDLSPSELAAQAW\$QKQGRARPS--DYRPT	259	
Dh	168	FNPAIDIEDTGNAYIVPHGGHYH1PKSDLSASELAAAKAHLA--GKNMQPSQLSYSST	224	
QY	260	PAPAPGRKAPIDVTPNPGQGHQDPDNGGYHPAPRRPNDA\$QNKHQ\$RDEFKGTPEKLLD	319	
Dh	225	PSPS-----LPI-----NPGTSHE-----KH-----	240	
QY	320	QLHRLDLKYRHAVEEDGLIFEPTQVIK\$NAFGYVVPHG\$HYH1IPRSQLSPLEME\$LDARY-	378	
Dh	241	-----EEDGYGF\$DANRIIAEDES\$GFVMSHG\$DHNHYEF\$K\$KDLTEEQ\$IKAAQ\$KHL	288	
QY	379	-----LAGQTEDD\$SG\$SDH\$KPSDK\$EVTHTFLGHR\$IKAYG\$KGLDGKPYDTS\$DA	426	
Dh	289	EEVKTS\$HNGLD\$LS\$H\$EQDYPSNAKEMKDL\$DK\$IEEK\$IAG-1MKQYGV-----KRES	339	
QY	427	YVESKESIH\$V\$DK\$SGVTAKHG\$DH\$HY-----IGF\$GEL-EQYELDEVANWV-KAKQO-	475	
Dh	340	IVVNKE-----KNAI1YPHG\$DHNHADPIDEHKPVG\$IGH\$SH\$NYELFKPEEGVAKK\$G\$NK	393	
QY	476	---ADELAALD-----QEQ\$KEK\$PLFD-----TKVS-----RKVTKDGKV	509	
Dh	394	VYTG\$EELTNVYNVLLKNSTFNMQNTLANGQ\$KRV\$SF\$PPELEK\$KL\$GIMLVKLITPD\$KV	453	
QY	510	GYMMPKDK\$KDY-----FYARDQ\$LDLTQ\$IAFAEQELM\$KDKKHRYD--1YDTGIEP	558	
Dh	454	--LEKVG\$KVG\$EG\$GVGNIAN\$FELDQ\$PYLP\$Q\$TF-KYTIASKDYPEVSYDGTFTVPTSLAY	510	
QY	559	RLAVDVSSLP\$M\$HAGNATYDTG\$S\$F\$V1PH-----IDH1H-----	591	
Dh	511	KMASQTI\$FY\$P\$F\$HAGD\$TYL\$RVNPQ\$FAV\$P\$K\$TDAL\$RVF\$DEF\$H\$NAYL\$ENNYKVG\$EIK\$LP1P	570	
QY	592	-----VVPY\$W\$LTR--DQATIKYVMOHPEVRPDI\$W\$K\$PGH\$E\$SG\$V1PNV-	635	
Dh	571	K1NQ\$T\$RTAGN\$K1P\$VTE\$MANAYL\$DNO\$T--Y1VEVP-----1LEKENQ\$TDKPS1PQ\$K	623	
QY	636	-----T\$PLDKRAGM\$PNWQ\$1IH\$SAEEYQK-ALAEGRFATPDGYI-----FDP-RDYVLAK	681	
Dh	624	RNKAQ\$EN\$K\$LD\$EK\$VEEPK-----T\$SEK\$VE\$KE\$K\$L\$SET\$GN\$T\$S\$N\$1LEEVPTVD\$P\$VQ\$EK\$YAK	678	
QY	682	--ET\$FVWK-----D\$G\$S\$1P\$RAD\$S\$S\$URT\$INK\$SDLSQ\$AEWQ\$Q\$AOELLAK\$KNAG\$DATD	731	
Dh	679	FAESY\$G\$M\$K\$LENVLEFNM\$DGTIELYLP\$SG\$EVI\$K-KMADFTGEARQ\$NGEN\$K\$P\$SENG\$K\$YSTG	737	
QY	732	T--DKP\$KEQ\$Q\$AD\$K\$SNENQ\$P\$SEASK\$E\$E\$K\$ESD\$FI-----D\$LPDYGL\$DRAT\$LED	780	
Dh	738	TVENQ\$PT\$ENK\$PAD\$SLPE--APNEK\$P\$YK\$PEN\$ST\$DNG\$MLN\$PEG\$NVG\$SDP\$MLD\$AL\$E\$E\$PAVD	795	
QY	781	H1NQ\$LAQK-----ANIDP\$KYLIFQ\$PEG-VQFY\$NKG\$ELV	813	
Dh	796	PVQ\$E\$K\$LEK\$T\$ASYGL\$GLDS-V1FNM\$DGTIELRLP\$SG\$EVI	833	

RESULT 9  
US-09-765-272-182  
; Sequence 182, Application US/09765272  
; Patent No. US20020061545A1

APPLICANT: Choi et. al.  
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
NUMBER OF SEQUENCES: 452  
CORRESPONDENCE ADDRESS:

```

; ADDRESSSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
;

```

OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/765,272  
FILING DATE: 22-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/961,083  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PB340P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 182:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 447 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 182:  
US-09-765-272-182

Query Match 19.2%; Score 839; DB 10; Length 447;  
Best Local Similarity 39.9%; Pred. No. 6.4e-52;  
Matches 178; Conservative 65; Mismatches 119; Indels 84; Gaps 10;

QY 25 LGKHHMGSAITKDNQAIYIDDSKGAAPKTKNTKMDQISAEQISAEQIVKTTDQGYVTS 84  
D 1 LNQHRSQENKDNRRVSYVDSQSQSKS--ENLTPDQVSQKEGIAEQIVIKITDQGYVTS 58  
QY 85 HGDHYHYNGKVPYDAIISELLMTDPNRYKQSDVINELDGYVIKNGNYVYLKPGS 144  
D 59 HGDHYHYNGKVPYDALFSEELMKDPNYQLKADIVNEVKGYIIVKVDKYYVYLKDA 118  
QY 145 KRKNIRTKQOIAEQVAKGTKEAKEGLAQAVALHLSKEEVAAVNEAKRQGRYTTDDGYIFSP 204  
D 119 HADNVRTKDEINRQKEHYKD-NEKVNNSVA-----VARSQGRYTTNDGYVFN 166  
QY 205 TDIDDLGDAYLVPHGNHYIIPKDLSPSELAAQAAYWSQKQGRGARPSPDPTAPAP 264  
D 167 ADIEDTGNAYIVPHGHYHYIPKSDLSASELAATAKAHLA---GKNMOPSOISYSTASD 223  
QY 265 GRRKAPIDVTPNPGQHPDNGGYHPAPRPNDASQNKQRDEFKGTRELLDQLHRL 324  
D 224 NNTQSVAKGSTSKPAN-----KSENIQSLKELLYDS 254  
QY 325 DLKRYHVEEDGLIFEPTQVYIKSNAFGYVPHGHYHIIPRSQLSPLEMELADRYL---A 380  
D 255 PSAQRYSESDGLVFPDAKIISRTPNGAIVPHGHYHFIPIYSKLSALEEKA-IRMVPISGT 313  
QY 381 GQTEDDDS-----GSDHSKPS---DKEVTHTEFLGHRIKAYGKGLDGKPYDTSDAY 427  
D 314 GSTVSTNAKPNEVVSSLSLSSPSLTTSKELS-----SASDGY 353  
QY 428 VESKESIHSDKSGVTAKHGDHFHYI 453  
D 354 IFNPKDIVEETATAYIVRHGDHFHYI 379

RESULT 10  
US-09-884-465A-381  
Sequence 381, Application US/09884465A  
Publication No. US20030077293A1  
GENERAL INFORMATION:  
APPLICANT: Shire Biochem, Inc.  
APPLICANT: Hamel, Josee  
APPLICANT: Brodeur, Bernard  
APPLICANT: Martin, Denis  
APPLICANT: Charland, Nathalie

APPLICANT: Ouellet, Catherine  
TITLE OF INVENTION: Streptococcus Antigens  
FILE REFERENCE: 055190-0044  
CURRENT APPLICATION NUMBER: US/09/884,465A  
CURRENT FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: 60/212,683  
PRIOR FILING DATE: 2000-06-20  
NUMBER OF SEQ ID NOS: 384  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 381  
LENGTH: 1238  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Unknown Organism  
NAME/KEY: MISC\_FEATURE  
LOCATION: (1)..(1)  
OTHER INFORMATION: Xaa = Methionine or nothing  
NAME/KEY: MISC\_FEATURE  
LOCATION: (430)..(430)  
OTHER INFORMATION: Xaa = Glycine or nothing  
NAME/KEY: MISC\_FEATURE  
LOCATION: (431)..(431)  
OTHER INFORMATION: Xaa = Proline or nothing  
US-09-884-465A-381

Query Match 10.3%; Score 451; DB 9; Length 1238;  
Best Local Similarity 19.7%; Pred. No. 1.4e-23;  
Matches 221; Conservative 150; Mismatches 312; Indels 440; Gaps 41;

QY 77 TDQGYVTSQHDHYHYNGKVPYDAIISELLMT----- 109  
D 36 TARGVAAPHGNHYH-----IPYEQMSELEKRIARIITPLRYSNHWPDSRPEEPSPOPTP 91  
QY 110 -----DENYRFKQSDVINEL-----DGYVIKNG-NYYVYLK----- 142  
D 92 EPSPSPQAPAPNPQAPAPSNPIDKLVKEAVRKVGDDGYVEENGVSRYIPAKNLSAETAAGI 151  
QY 143 -----GSKRKN-----RTKQOIAEQVAKGT--EAKK 169  
D 152 DSKLAKQESLSHKLGAKKTDLPSSDREFYKAYDLARHQDLDN--KGRQVDFEALDN 209  
QY 170 GLAQVAHLSKEEVAAVNE-----AKRQGRYTTDDG 199  
D 210 LLERLKDVSSDKVKLVLDILAFLAPIRHPERLGKPNQAITYTDEIQVAKLAGKYTTEG 269  
QY 200 YIFSPDTIDDLGDAYLVPHGNHYIIPKDLSPSELAAQAAYWSQK----- 246  
D 270 YIFDPRDITSDGDAYVTPHMTSHWIKKDSLSEAEERAAQAAYAKEKGLTPSTDHQDSG 329  
QY 247 --QGRGARPSPDPTAPAPAPGRKAPIDVTPNPGQHPDNG----- 287  
D 330 NTEAKGAELIYNRVKAA-----KVPFLDRMPYNLQYVEYKNGSLIIPHYDHNKFEW 384  
QY 288 ---GYHPAP-----PRPD-----A 299  
D 385 FDEGLYEAPKGYTLEDLLATVYVEHPNERPHSDNGFGNASDVXXNMOPSOISYSTA 444  
QY 300 SQNKHQ-----RDEFKGTRELLDQLHRLDLKRYHVEEDGLIFEPTQVYIKSNAFGY 351  
D 445 SDNNTQSVAKGSTSKPANKEENLQSLKELLYDSPAQRYSSESDGLVFPDAKIISRTPN 504  
QY 352 VPHGDHYHIIPRSQLSPLEMELADRYL---AGQTEDDDS-----GSDHSKPS-- 396  
D 505 ALPHGDHYHFIPIYSKLSALEEKA-IRMVPISGTGSTVSTNAKPNEVVSSLSLSSPSLT 563  
QY 397 --DKEVTHTEFLGHRIKAYGKGLDGKPYDTSDAYVFSKESIHSDKSGVTAKHGDHFHYI- 453  
D 564 TTSKELS-----SASDGYIFNPKDIVEETATAYIVRHGDHFHYIP 603  
QY 454 GFGELEQYELDEVANWVAKAGQADELAALDQEQKEKPL-FDTKKVSRKVTGDKVGYM 512  
D 604 KSNQIGQPTLPN--NSLATPSPSLPINPGTSHKHEEDGCGFD---ANRIIAEDESG 657



QY 513 MPKDGKDYFYARDQDLTQIAFAEQLMLKDKKHRYDI-----VDTG 555  
 Db 658 MSHGDHNNHYFFKKDLTEEOIKAAQKHLEEVKTSNGLDLSLSEODYPGNAKEMKDLDDK 717  
 QY 556 IEPRLAVDVSSLPMHAGNATYDTGSSFYI-PHIDHIVVPYSLTRDQIAT-----K 607  
 Db 718 IEEKIAGIMKQYGVKRESIVVNKEKNATIIYPHGDHHDPI-----DEHKPVGIGSHSN 772  
 QY 608 YVMQHPPEVRPDIMSKPGHE-ESGSVIPNVTPLDKRAGMPNWI-----IHSAEV 656  
 Db 773 YELFKPE--EGVAKKEGKNVYTGELTNVNLKNSFTNNONFTLANGQKRVSEFSFPEL 830  
 QY 657 QKALAEQ---RFATPDGYIFD-----PRDLAKETP----- 684  
 Db 831 EKKLGIMLVKLITPDGKYLEKVSQKVFEGVGNIANFELDQPYLPQOTFKYTIASKDYP 890  
 QY 685 -VMKDSFSIPRA----- 696  
 Db 891 EVSIDGTFTVPTSLAYKMASQTIFFYPFHAGDTYLRVNPQFAVPKGTDALVRVDEFHGNA 950  
 QY 697 -----DGSSLRTINKSDL-----SQAEWQAQELLAKKNAGD 728  
 Db 951 YLENNYKVGEEKLPKPLNCGTTRTAGNKIPVTFMANAYLDNQSTYIIVEVPILEKEN--- 1007  
 QY 729 ATDTDKP-----KEQQAQDKSNENQOPSEASKKEKE-----SDDFIDSLDPY 771  
 Db 1008 -QTDKPSILPQFKRNKAQENSKLDEKVEEPTSEKYEKELSETGNSNSTLEEVPTV 1065  
 QY 772 GLDRATLEDHINOLAQKANIDPKYLIPOEG-VQFYKNGELV 813  
 Db 1066 D---PYQEKVAKFAESYGMKLENVLFNMDGTIELYLPSEGEV 1104

RESULT 11  
 US-09-884-465A-382  
 : Sequence 382, Application US/09884465A  
 : Publication No. US2003007293A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Shire Biochem, Inc.  
 : APPLICANT: Hamel, Josee  
 : APPLICANT: Brodeur, Bernard  
 : APPLICANT: Martin, Denis  
 : APPLICANT: Charland, Nathalie  
 : APPLICANT: Ouellet, Catherine  
 : TITLE OF INVENTION: Streptococcus Antigens  
 : FILE REFERENCE: 055190-0044  
 : CURRENT APPLICATION NUMBER: US/09/884,465A  
 : PRIOR FILING DATE: 2001-06-20  
 : PRIOR APPLICATION NUMBER: 60/212,683  
 : NUMBER OF SEQ ID NOS: 384  
 : SOFTWARE: PatentIn version 3.1  
 : SEQ ID NO 382  
 : LENGTH: 1365  
 : TYPE: PRT  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: Unknown Organism  
 : NAME/KEY: MISC\_FEATURE  
 : LOCATION: (1)..(1)  
 : OTHER INFORMATION: Xaa = Methionine or nothing  
 : NAME/KEY: MISC\_FEATURE  
 : LOCATION: (557)..(557)  
 : OTHER INFORMATION: Xaa = Glycine or nothing  
 : NAME/KEY: MISC\_FEATURE  
 : LOCATION: (558)..(558)  
 : OTHER INFORMATION: Xaa = Proline or nothing  
 : US-09-884-465A-382

Query Match 9.3%; Score 406.5; DB 9; Length 1365;  
 Best Local Similarity 17.8%; Pred. No. 2.4e-20;  
 Matches 222; Conservative 156; Mismatches 310; Indels 557; Gaps 43;

QY 77 TDQGYVTSHGHHFYNGKVPYDAIISELLMT----- 109  
 Db 36 TARGVAVPHGNHYHF---IPYEQMSELEKRIARIIPLRYSNHWVDRSPREESPQPTP 91  
 QY 110 -----DPNRYFKQSDVINEL-----DGYVIKVNQ-NYYVYLKP----- 142  
 Db 92 EPSPPQAPNPQAPAPSNPIDELKVAVRKVGDSGYFEENGVSRYIPAKNLSAETAAGI 151  
 QY 143 -----GSKRKN-----RTKQIAEQVAKGK---EAKK 169  
 Db 152 DSKLAKQESLSHKLGAKKTDLPSSDREFYKNKAYDLLARIHQDLLDN--KGRQVDEEALDN 209  
 QY 170 GLAQVAHLSKEEVAANE-----AKRQRYTTDDG 199  
 Db 210 LLERLKVSSDKVKLVDDILAFILRHPERLGFPAQIITYTDEIQVAKLAGKTTEDG 269  
 QY 200 YIFSPYDIDLDGDAYLVPHGNHYHYIPKDLSPSELAAQAYWSQK----- 246  
 Db 270 YIFDPRDITSDEGDAYVTPHMTHSHWIKKDSLSEAEARAQAAYAKEKGLTPPSTHQDSG 329  
 QY 247 --QGRGA----- 251  
 Db 330 NTEAKGAELIYNRVKAACKVPLDRMPYNLYQTVVEVKNGLIIPHYDHYNIKFEWEDEGL 389  
 QY 252 -----RPSDYR 257  
 Db 390 YEAPKGYTLEDLLATVKYVEHPNERPHSDNGFGNASDHYQRNKNQADTNTQTEKPSSEK 449  
 QY 258 P-----TP--APARGKAPIPDVT--NPGQHQP----- 284  
 Db 450 POTEKPEETPREEKPOSEKPESPKPEEPPEESPESEEPQVETEKEVEKLEAEEDLLG 509  
 QY 285 -----DNG-----GYHAPRRPND 298  
 Db 510 KIQDPIIKSNAKETLTGLKNNLLFGTDQDNTIMAEAEKLLALLKESKXXNMQPSQLSYSS 569  
 QY 299 ASQNKHQDEREKGTKE-----ELLDQLRLDLKYRHYEEDGLIFEPTQVIXSNAF 349  
 Db 570 TASDNTQSVAKGSTSKPANKSENLOSLEKELYDSPAQRYSSEDGLVFDPAKIISRTFN 629  
 QY 350 GYVVPHGHHYHIIIPRSQSLPEMELADRYL---AGQTEDDDS-----GSDHSKPS 396  
 Db 630 GVAIPHGDHYYHIFYSKLSALEKIA-RMVPISGTGSTVSTNAKNEVSSLSGSSNPS 688  
 QY 397 ---DKEVHTFTFLGRIRIKAYGKGLDGKPYDTSDAYVESKESHSYDKSQVTAKHGDHFI 452  
 Db 689 SLTTSKELS-----SASDGYIIFNPKDIVEETATAYIVRHGDHFI 728  
 QY 453 I-GFGELEQYELDEVANWVAKAGQADELAALDQOGEKPL-FDTKKVSRYTKDGKYG 510  
 Db 729 IPKSNQIGQPTLPN--NSLATPSPSLPINDGTSHEKHEDGYGFD---ANRIIAEDES 782  
 QY 511 YMPKDGKDYFYARDQDLTQIAFAEQLMLKDKKHRYDI-----VD 553  
 Db 783 FVMSHGDHNNHYFFKKDLTEEOIKAAQKHLEEVKTSNGLDLSLSEODYPGNAKEMKDLDD 842  
 QY 554 TGEPRLAVDVSSLPMHAGNATYDTGSSFYI-PHIDHIVVPYSLTRDQIAT----- 606  
 Db 843 KIEEKIAGIMKQYGVKRESIVVNKEKNATIIYPHGDHHDPI-----DEHKPVGIGSH 897  
 QY 607 -KYVMQHPPEVRPDIMSKPGHE-ESGSVIPNVTPLDKRAGMPNWI-----IHSAE 654  
 Db 898 SNYELFKPE--EGVAKKEGKNVYTGELTNVNLKNSFTNNONFTLANGQKRVSEFSFPP 955  
 QY 655 EVQKALAEQ---RFATPDGYIFD-----PRDLAKETP----- 684  
 Db 956 ELEKKLGIMLVKLITPDGKYLEKVSQKVFEGVGNIANFELDQPYLPQOTFKYTIASKD 1015  
 QY 685 -VMKDSFSIPRA----- 696  
 Db 1016 YPEVSYDGTFTVPTSLAYKMASQTIFFYPFHAGDTYLRVNPQFAVPKGTDALVRVDEFHG 1075

QY 697 -----DSSSLRTINKSDL-----SQAEWQAQELLAKKNA 726  
DB 1076 NAYLENNYKVEIKLPIPKLNOGTTTRAGNKIPVTFMANAYLDNOSTYIVEVPILEKEN- 1134  
QY 727 GDATAIDTKP-----KEKQADKSNENQPSSEASKKEEKE-----SDDFIDSLP 769  
DB 1135 ----QTDKRSILPQFKRNKAQENSKLDEKVEEPKTSKEKEKLESETGNTSTNSSTLEEV 1190  
QY 770 DYGDLRATLEDHINOLAQKANIDPKYLIQPEG-VQFYNNKNGELV 813  
DB 1191 TVD-----PVQEKVAKFAESYGMKLENVLFNMDGTIELYLPSEGEVI 1231

## RESULT 12

US-09-884-465A-378  
; Sequence 378, Application US/09884465A  
; Publication No. US20030077293A1  
; GENERAL INFORMATION:  
; APPLICANT: Shire Biochem, Inc.  
; APPLICANT: Hamel, Josee  
; APPLICANT: Brodeur, Bernard  
; APPLICANT: Martin, Denis  
; APPLICANT: Charland, Nathalie  
; APPLICANT: Ouellet, Catherine  
; TITLE OF INVENTION: Streptococcus Antigens  
; FILE REFERENCE: 055190-0044  
; CURRENT APPLICATION NUMBER: US/09/884,465A  
; PRIOR FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: 60/212,683  
; NUMBER OF SEQ ID NOS: 384  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 378  
; LENGTH: 1378  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Unknown Organism  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: Xaa = Methionine or nothing  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (570)..(570)  
; OTHER INFORMATION: Xaa = Glycine or nothing  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (571)..(571)  
; OTHER INFORMATION: Xaa = Proline or nothing  
US-09-884-465A-378

Query Match 8.9%; Score 390.5; DB 9; Length 1378;  
Best Local Similarity 17.6%; Pred. No. 3.4e-19;  
Matches 221; Conservative 149; Mismatches 318; Indels 569; Gaps 42;

QY 77 TDQGYVTSBGHGHFYNGKVPYDAIISSE----- 105  
DB 37 TARGVAVPHGNHYH-----IPYEQMSELEKRIARIIPLRYSNHWVPDSRPEQSPQSTP 92  
QY 106 ----LMTDPNRYFKQSDVINEL-----DGYVIKVGNG-NYYVYLKP----- 142  
DB 93 EPSPSLQAPNPQAPSNPIDKLVKAVRKVDGYVEENGVSRYIPAKDLSAETAAGI 152  
QY 143 -----GSKRKNI-----RTKQIAEQVAKGTK---EAKK 169  
DB 153 DSKLAKQESLSHKLGAKKTDLPSSDREFYNAKYDLLARIHQDLIDN--KGRQVDFEVLN 210  
QY 170 GLAQVAHLSKEEVAANE-----AKRQGRYTTDDG 199  
DB 211 LLERLKDVSSDKVKLVYDILAFAPIRHPERLCKPNAQITTYTDEIQVAKLAGKYYTTEDEG 270  
QY 200 YIFSPTDIIDLDGDAYLVPHGNHYHYIPKDKLSPSELAQAAYWSQK----- 246  
DB 271 YIFDPRDITSDEGDAYVTPHMTSHWIKKDSLSAERAAQAAYAKKEGILTPPSTDHQDSG 330

QY 247 --QGRGAR----- 252  
DB 331 NTEAKGAFAIYNRYKAACKVPLDRMPYNLQYTVWEKNGSLIIPHYDHYHNKIFEWFEDEGL 390  
QY 253 ---PSDY-----RPTPAPAPG-----RRKAPIDPVTNPGQGHQPD 285  
DB 391 YEAPKGSLEDLLATVKKYVEHPNERPHSDNGFGNASDHYVRKNKADQDSKPDEDEKHEDEV 450  
QY 286 NGCYHP----- 291  
DB 451 SEPTHPESDEKENHAGLNPADNLKYPSTDTETEEDTDEAETIPEQVENSVINAKIA 510  
QY 292 -----APRP----- 296  
DB 511 DAELALLEKVTDPSTRONAMETLTGLKSSLLGTRKDNNTISAEVDSLLALLKESQAPIQX 570  
QY 297 -----NDASQNKHO-----RDEFGKTFKELLDDQLHRLDLKYRHAVEEDGLI 337  
DB 571 XNMQPSQLSYSTASDNNTQSVAKGSTSKPANKSENLOSLLKELYDSBSAQRYSESGLV 630  
QY 338 FEPTQVIXSNAFGYVPHGDHYIIPRSQSPLEMLADRYL---AGQTEDDDS----- 388  
DB 631 FDPAKIISRTPNQVAIPHGDHYHEIPYSKLSALEKIA-RMVPISGTGSTVSTNAKPNEV 689  
QY 389 ----GSDHSKPS---DKEVTHTEFLGHRIKAYGKLDGKPYDTSDAYVESKESHSVDKS 440  
DB 690 VSSLGSLSSNPSSLTTSKELS-----SASDGYIENPKDIVEETAT 729  
QY 441 GVTAKHGDHFHYI-GFGELEQYELDEVANWVKAKGADELAAALDQEQKEKPL-FDTKK 498  
DB 730 AIVRHGDHFHYIPKSNQIQPTLPN--NSLATPSPSLPINPGTSHEKHEEDGYGFD--- 784  
QY 499 VSRKVTKDGKVGVMPPKDKGYFAYARDQLDTQIAFAEQELMLKDKKHRYDI----- 551  
DB 785 -ANRIIAEDESGFVMSHGDHNYHFFKKDLTEEQIKAAQKHLEEVKTSHNGDLSLSHEQD 843  
QY 552 -----VDTGIEPRLAVDVSSLPMAHGNATYDTGSSFYI-PHIDHIHVVPYSWLT 600  
DB 844 YPGNAKEMKDLDKKIEEKIAGIMKQYGVKRESIYVNAKKNALIIYPHGDHNDPI----- 898  
QY 601 DQIATI-----KYVMQHPVPRDIWSKPGHE-EGSVIPIVNTPLDKRACMPNQOI--- 649  
DB 899 DEHKRVGIGHSNHYELFKPE--EGVAKKEGKNKYTGEBELTNVNLKNSFTNNQNTLA 956  
QY 650 -----IHSAEEVOKALAE--REFATPDGYIFD-----PRDVLA 680  
DB 957 NGQKRVSEFPEPELEKKGILGIMLVKLITPDGKLVLEKVGKVEGEGVNIANFELDQPYLP 1016  
QY 681 KETF-----VWKDGSFSIPRA----- 696  
DB 1017 GQTFKYTIASKDYPEVSIDGFTVPTSLAYKMASQTIFFPHAGDTYLRVNPQFAVPKGT 1076  
QY 697 -----DSSSLRTINKSDL-----SQAEW 714  
DB 1077 DALVRVDEFHGNAYLENNYKVEIKLPIPKLNOGTTTRAGNKIPVTFMANAYLDNOSTY 1136  
QY 715 QQAQELLAKKNAGDATIDTKP-----KEKQADKSNENQPSSEASKKEEKE----- 760  
DB 1137 IVEVPILEKEN-----QTDKRSILPQFKRNKAQENSKLDEKVEEPKTSKEKEKLESETG 1191  
QY 761 ---SDDFIDSLPDYGLDRATLEDHINOLAQKANIDPKYLIQPEG-VQFYNNKNGELV 813  
DB 1192 NSTNSTLEEVPVTV--PVQEKVAKFAESYGMKLENVLFNMDGTIELYLPSEGEVI 1244

## RESULT 13

US-09-884-465A-377  
; Sequence 377, Application US/09884465A  
; Publication No. US20030077293A1  
; GENERAL INFORMATION:  
; APPLICANT: Shire Biochem, Inc.  
; APPLICANT: Hamel, Josee  
; APPLICANT: Brodeur, Bernard

APPLICANT: Martin, Denis  
APPLICANT: Charland, Nathalie  
APPLICANT: Ouellet, Catherine  
TITLE OF INVENTION: Streptococcus Antigens  
FILE REFERENCE: 055190-0044  
CURRENT APPLICATION NUMBER: US/09/884,465A  
CURRENT FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: 60/212,683  
PRIOR FILING DATE: 2000-06-20  
NUMBER OF SEQ ID NOS: 384  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 377  
LENGTH: 999  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Unknown Organism  
NAME/KEY: MISC\_FEATURE  
LOCATION: (1)..(1)  
OTHER INFORMATION: Xaa = Methionine or nothing  
NAME/KEY: MISC\_FEATURE  
LOCATION: (570)..(570)  
OTHER INFORMATION: Xaa = Glycine or nothing  
NAME/KEY: MISC\_FEATURE  
LOCATION: (571)..(571)  
OTHER INFORMATION: Xaa = Proline or nothing  
US-09-884-465A-377

Query Match 8.2%; Score 359.5; DB 9; Length 999;  
Best Local Similarity 22.3%; Pred. No. 3.5e-17;  
Matches 180; Conservative 114; Mismatches 282; Indels 231; Gaps 37;

QY 60 QISAEGISAEQIVKTDQGYVTSBGDHYHNGKVPYDAIISBELMTDPNY----- 113  
DB 260 QFAVPGKGTDA---LVRFVDE---FHGNAYLENNYKV-----GEIKLPIPKLNQGTTR 305  
QY 114 ---RFKQSDVINEILDG---YVIKV-----NGNYVYLKPGSKRKNIKTQOIAEQV- 159  
DB 306 TAGNKIPVTFMANAYLDNOSTYIVEVPILEKENQTDKPSILPQFRNKQAQENSKLDEKVE 365  
QY 160 -AKGTKEAKEKGLAQAHLKSK---EEVAANVNAKRQ-GRYTTDDGY----- 200  
DB 366 EPKTSKVEKEKLESTGNSTNSTLEEVPTVDVQEKVAKFAESYGMKLENVLFNMDGTI 425  
QY 201 -IFSPT-----DIIDLDGDAYLVPHGNHYHYIPKKDLSPESELAQAQYWSQKQGRGARP 253  
DB 426 ELYLPSEGEVIKKNMADFTGEA---PQGN-----GENKPSENGKYSTGTVENQPTENKP 475  
QY 254 SDYRPTPAPAPGRKKAPI-PDVTNPNQCGHQPDNGGYHP-----APP----- 294  
DB 476 ADSLP---EAPNEK--PVKPNSTDMGMLNPEGNVGSDPMLDPALEAPAVDPVQEKLEK 530  
QY 295 -----RPNDASQNKHQRDEFKGTKEKLLDQLHRLDLKRYRHV 331  
DB 531 FTASYGLDSDVIFNMDGTIELRLPSGEVIKKNLSDFIAXXDIDSLKQLYKPLSQRHV 590  
QY 332 EEDGLIFEPTQVIKSNAGYVVPBGDHYHIIPRSQLSPELMELAD---RYLAGQTEDD 387  
DB 591 ESDGLIFBPAQITSRTARGAVALPHGNHYHFIPEQMSLEKRIARIILRLYRSNNHWVPD- 649  
QY 388 SGSDHSKPSDKEVTHTEFLGRIKAYGKGLDGKPYDTSDAYVFSKESISHVDSKSGVTAKHG 447  
DB 650 --SRPEEPSQPTPEPSPSPQAPAPNPQAPSPNPIDEK---LVKEAVRV-----G 694  
QY 448 DHFHYIGFELEQYELDEVANVNAKQAQADELAALDQEQKEKPLFDTKKVSRYKVRDG 507  
DB 695 DGY-----VFEENGVSRYTPAKNLSAETAAGIDSKLAKQESL--SHKLGAKTID-- 741  
QY 508 KVGYNMPPKDGKDYFYARDQLDLTQIAFAEQELMLKDKKHRYRYDIVDTGIEPRLAVDVSSL 567  
DB 742 -----LPSSDREFY--NKAYDL--LARIHQDLDNKGRQYDPEALDNLE-RLK-DVSS- 789  
QY 568 PMHAGNATYDTGSSSFVIPHIDHIVVPSWLTTRDQIATIKYVMQHPEVRPDIVSKPGHEE 627

DB 790 -----DKVKLV-----DILAFLAPIRHPE----- 809  
QY 628 SGSVIPNVTPLDKRAGMPNWOIHSAEVQKALAEGRFATPDGYIFDPRLAKETFWVK 687  
DB 810 -----RLGKPNAITTYTDDIEIQVAKLAGKYTTEDGYIFDPRDITSDE----- 851  
QY 688 DGSFISPRADGSSLRITNKSLSQAQEWQAQELLAKKNAGDATDTDKPKKQADKSNEN 747  
DB 852 GDAYVTPHMTHS--HWIKKDSLSEAEERAAQAAYAKEKGL-----TPPSTDHQDSGNT 902  
QY 748 QQPSSEASKEEKEKESDDF-IDSLPDYGL 773  
DB 903 AKGAFAIYNRVKAKKVPDIDRMP-YNL 928

RESULT 14  
US-09-884-465A-379  
Sequence 379, Application US/09884465A  
Publication No. US20030077293A1  
GENERAL INFORMATION:  
APPLICANT: Shire Biochem, Inc.  
APPLICANT: Hamel, Josee  
APPLICANT: Brodeur, Bernard  
APPLICANT: Martin, Denis  
APPLICANT: Ouellet, Catherine  
TITLE OF INVENTION: Streptococcus Antigens  
FILE REFERENCE: 055190-0044  
CURRENT APPLICATION NUMBER: US/09/884,465A  
CURRENT FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: 60/212,683  
PRIOR FILING DATE: 2000-06-20  
NUMBER OF SEQ ID NOS: 384  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 379  
LENGTH: 1152  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Unknown Organism  
NAME/KEY: MISC\_FEATURE  
LOCATION: (1)..(1)  
OTHER INFORMATION: Xaa = Methionine or nothing  
NAME/KEY: MISC\_FEATURE  
LOCATION: (344)..(344)  
OTHER INFORMATION: Xaa = Glycine or nothing  
NAME/KEY: MISC\_FEATURE  
LOCATION: (345)..(345)  
OTHER INFORMATION: Xaa = Proline or nothing  
US-09-884-465A-379

Query Match 8.2%; Score 359; DB 9; Length 1152;  
Best Local Similarity 20.7%; Pred. No. 4.7e-17;  
Matches 196; Conservative 138; Mismatches 290; Indels 322; Gaps 50;

QY 32 SATKDNQIAYIDSKGKAKAPKTNT-----MDQISAEGISAEQIV-----VK 75  
DB 356 STASDNNTQSV--AKGSTSKP--ANKSENLOSLLKELYDSPSAQRYSESDDGLVDPKAITIS 412  
QY 76 ITDQGYVTSBGDHYHNGKVPYDAIIS--ELLMTDPNRYRFKQSDVINELDGYVIKVG 134  
DB 413 RTPNGVAIPHGDHYHF---IPYKLSALEBEKI-----ARMVPISG 449  
QY 135 NYVYLKPGSKRKNIKTQOIAEQVAK-GTKEAKEKGLAQAHLKKEEVAANVNAKRQGR 193  
DB 450 T-----GS--TVSTNAKPNEVSVSLGSLSSNPSSLTTSKELS----- 484  
QY 194 YTTDDGYIFSPDITIDLDGDAYLVPHGNHYHYIPKKDLSPESELAQAQYWSQKQGRGARP 253  
DB 485 -SASDGYIFNPKDIVEETATAYIVRHGDHFHYIPK-----SNQIGQPTLP 528  
QY 254 SDYRPTPAPAPGRKKAPIPDVTNPNQCGHQPDNGGYHPAPRPNDASQNKHQRDEFKGT 313



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Db 529 NNSLATSPS-----LPI-----NPGTSHE-----KH----- 550
QY 314 FKELLQHLRLDLKYRHEEDGLIFPTQVKSNAFGYVVPBGDHYHIIIPRSQSPLEME 373
Db 551 -----EEDGYGFANRIIAEDESSEFVMSGDHNYFFKKDLTEEQIK 592
QY 374 LADRY-----LAGQTEDDSGSDHSPSKDEVTHTFLGHRIKAYGKGLDGR 420
Db 593. AAOQHLEEVKTSNGLDLSLSDHEDYPCGNAKEMKDLDKITEKIAIG-IMKQYV----- 645
QY 421 YDTSDAVFSKESHSVDKSGVTAKHGDFHY-----IGFGL-EOYELDEVANWY- 470
Db 646 --KRESIVNKE-----KNATIPYHGDHHDADPIDEHKPVGIGHSHSNYELFKPEGVA 697
QY 471 KAKQ-----ADELAALD-----QEOGKEKPLFD-----TKKVS-----RKV 503
Db 698 KKEGNKYTGEELTNVNLKSNSTFNNQNTLANGQKRVSEFPPELEKKLGINMLYKLI 757
QY 504 TKDGKGYMPPKDKDY-----FYARDQDLTQIAFAEQELMLKDKKHRYD-----IV 552
Db 758 TPDGKY--LEKVSQKVFEGEGVGNIANFELDQYLPQGF- KYTIASKDYPEVSVDGTFYV 814
QY 553 DTGIEPRLAVDVSSLPMAHAGNATYDTGSSFVIRH-----IDHIH----- 591
Db 815 PTLAYKMASQTIYFPHAGDTYLRVNPQFAVPKGTDALVRVDEFHGNAYLENNYKVG 874
QY 592 -----VVPYSWLTIR--DQIATIKYVMQHPEVRPDIWSKPGHEESGS 630
Db 875 IKLPIPKLNGOTTRTAGNKIPVTFMANAYLDNOST--YIVEVP-----ILEKENQTDKPS 927
QY 631 VIPNV-----TPLDKRAGMPNWQIIHSAEEVOK-ALAEGRFATPDGYI-----FDP- 675
Db 928 ILPOEKRNKAQENSKLDEKVEERK-----TSEKVEKEKLESETGNSTNSTLEEVPTVDPV 982
QY 676 RDVLAK--ETFWK-----DGSFISPRADGSSLRTINKSDLSQAEMQOAOELLAKKN 725
Db 983 QEKYAKFAESYGMKLENVLFNMDGTIELYLPSEGEVIK-NMADFTGEAPQNGENKPS 1041
QY 726 AGDATDT--DKPEKQOADSNNQOPEASEKKEESDDFI-----DSLDPDGLD 774
Db 1042 GKYSTGTVENQPTENKPADSLPE--APNEKPVKPESTNDGMLNPEGNVGSDPMDLPALE 1099
QY 775 RATLEDHINOLAQK-----ANIDPKYLIFQPEG-VQFYNNKNGELY 813
Db 1100 EAPAVDPVQEKLEKFTASYGLGLDS--VIFNMDGTIELRLPSGEVI 1143

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RESULT 15
US-09-884-465A-383
; Sequence 383, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 383
; LENGTH: 1126
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism

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; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa = Methionine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (557)..(557)
; OTHER INFORMATION: Xaa = Glycine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (558)..(558)
; OTHER INFORMATION: Xaa = Proline or nothing
US-09-884-465A-383

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Query Match 7.8%; Score 341; DB 9; Length 1126;  
 Best Local Similarity 25.0%; Pred. No. 8.8e-16;  
 Matches 138; Conservative 66; Mismatches 177; Indels 170; Gaps 23;

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QY 317 LLDQLHLRLDLKYRHEEDGLIFPTQVKSNAFGYVVPBGDHYHIIIPRSQSPLEMLAD 376
Db 6 LKQLYKLPLSQRHYESDGLIFDPAQITSRITAGVAVPHGNHYHFIPEOMSELEKRIAR 65
QY 377 ----RYLAGQTEDDSGSDHSPSKDEVTHTFLGHRIKAYGKGLDGRPYDTSDAYVFSKE 432
Db 66 IIPLRYSNHWVPD--SRPEEPSQPTPEPSPSPQAPNPQAPSNPIDEK---LVKE 118
QY 433 SIHSVDKSGVTAKHGDFHYIGFGELEQYELDEVANWVKAKQOADELAALDQEGKEKP 492
Db 119 AVRKV-----GDGY-----VEENGVSRYIPAKNLISATTAAGIDSKLAKQES 160
QY 493 LFDTKKVSRYKVTGDKGVYMPKDKGKYFYARDQDLTQIAFAEQELMLKDKKHRYDIY 552
Db 161 L--SHKLGAKKTD-----LPSSDREFY--NKAYDL--LARIHQDLLDNKGRQVDFEAL 207
QY 553 DTGIEPRLAVDVSSLPMAHAGNATYDTGSSFVIRPHIDHIHVVPYSWLTIRQIATIKYVMQH 612
Db 208 DNLE-RLK-DVSS-----DKVKLV-----DDLAF LAPIRH 237
QY 613 PEVRPDIWSKPGHEESGSVIPNVTPLDKRAGMPNWQIIHSAEEVOKALAEGRFATPDGYI 672
Db 238 PE-----RLGKPNQAQITTYTDEIQVAKLAGKYTTEDGYI 271
QY 673 FDPRLVAKETFWKDGFSFISPRADGSSLRTINKSDLSQAEMQOAOELLAKKNAGDATDT 732
Db 272 FDPRLDITSDE-----GDAYVTTPHMTHS--HWIKKDSLSEAEARAAQAYAKEKGL----- 318
QY 733 DKPEKQOADSNNQOPEASEKKEESDDFI-IDSLP----- 769
Db 319 -TPPSTDHQDSGNTPEAKGAELIYNNRYKAARKVPLDRMPYNLQYTVVEVKNGLIIPHYDH 377
QY 770 -----DYGLDRA--TLEDHINOLAQKANIDPKYLIFQ-----EGV 803
Db 378 HNIKFEWFDEGDIYEAPKGYTLEDLATV-----KYVEHNERPHSDNGFGNASDHY 429
QY 804 QFYNNKNGELVT 814
Db 430 Q-RNKNQQADT 439

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Search completed: May 19, 2003, 08:23:52  
 Job time : 249.022 secs



GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 19, 2003, 07:51:03 ; Search time 12.8853 Seconds

(without alignments)  
1883.841 Million cell updates/sec

Title: US-09-645-835A-2  
Perfect score: 4376  
Sequence: 1 VKKTYGYIGSVAAILLATHI.....YKNKGELVTVYDIKTLQGINP 825

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1032	23.6	763	4	US-08-961-083-66	Sequence 66, Appl
2	949	21.7	796	4	US-08-961-083-56	Sequence 56, Appl
3	839	19.2	447	4	US-08-961-083-182	Sequence 182, App
4	143.5	3.3	1861	2	US-08-790-912-4	Sequence 4, Appli
5	142.5	3.3	1588	5	PCT-US93-07261-11	Sequence 11, Appl
6	142.5	3.3	1663	5	PCT-US93-07261-16	Sequence 16, Appl
7	133	3.0	2465	2	US-08-596-291-3	Sequence 3, Appli
8	133	3.0	2465	3	US-09-100-804-3	Sequence 3, Appli
9	131.5	3.0	1541	4	US-08-296-791-3	Sequence 3, Appli
10	131.5	3.0	1541	5	PCT-US95-10661A-3	Sequence 3, Appli
11	129	2.9	893	4	US-09-514-302-4	Sequence 4, Appli
12	129	2.9	1938	4	US-09-514-302-2	Sequence 2, Appli
13	128.5	2.9	1076	2	US-08-867-941-19	Sequence 19, Appl
14	128.5	2.9	1076	4	US-09-074-658-19	Sequence 19, Appl
15	127	2.9	765	2	US-08-663-112-2	Sequence 2, Appli
16	127	2.9	783	6	5231168-2	Patent No. 5231168
17	125	2.9	10182	4	US-09-134-001C-3159	Sequence 3159, Ap
18	124	2.8	706	4	US-09-059-584-46	Sequence 46, Appli
19	124	2.8	1848	4	US-08-296-791-6	Sequence 6, Appli
20	124	2.8	1848	5	PCT-US95-10661A-6	Sequence 6, Appli
21	123.5	2.8	2366	1	US-08-480-604A-10	Sequence 10, Appl
22	123.5	2.8	2366	2	US-08-405-496A-10	Sequence 10, Appl
23	123.5	2.8	2366	4	US-08-915-136-10	Sequence 10, Appl
24	123.5	2.8	2366	4	US-08-957-310-10	Sequence 10, Appl
25	121.5	2.8	1702	4	US-08-296-791-5	Sequence 5, Appli
26	121.5	2.8	1702	5	PCT-US95-10661A-5	Sequence 5, Appli
27	121	2.8	506	3	US-09-032-365A-19	Sequence 19, Appl

28	121	2.8	608	1	US-08-480-604A-21	Sequence 21, Appl
29	121	2.8	608	2	US-08-405-496A-21	Sequence 21, Appl
30	121	2.8	608	4	US-08-915-136-21	Sequence 21, Appl
31	121	2.8	608	4	US-08-957-310-21	Sequence 21, Appl
32	121	2.8	609	1	US-08-480-604A-30	Sequence 30, Appl
33	121	2.8	609	4	US-08-915-136-30	Sequence 30, Appl
34	121	2.8	2466	3	US-09-080-855-12	Sequence 12, Appl
35	121	2.8	2466	5	PCT-US94-09943-2	Sequence 2, Appli
36	120.5	2.8	542	1	US-08-701-380-2	Sequence 2, Appli
37	120.5	2.8	542	3	US-09-032-365A-13	Sequence 13, Appl
38	120.5	2.8	747	1	US-07-854-596B-40	Sequence 40, Appl
39	120.5	2.8	1151	4	US-09-134-001C-3242	Sequence 3242, Ap
40	120.5	2.8	1181	2	US-08-488-940-2	Sequence 2, Appli
41	120	2.7	2485	4	US-09-290-640-46	Sequence 46, Appl
42	117.5	2.7	672	3	US-09-040-843-4	Sequence 4, Appli
43	117.5	2.7	672	4	US-09-621-855-4	Sequence 4, Appli
44	117.5	2.7	823	4	US-09-134-001C-4081	Sequence 4081, Ap
45	117.5	2.7	866	3	US-09-040-843-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-08-961-083-66  
Sequence 66, Application US/08961083  
Patent No. 6159469  
GENERAL INFORMATION:  
APPLICANT: Choi et. al.  
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
NUMBER OF SEQUENCES: 452  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961,083  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PB340P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 763 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-961-083-66  
Query Match 23.6%; Score 1032; DB 4; Length 763;  
Best Local Similarity 33.6%; Pred. No. 1.8e-75;  
Matches 285; Conservative 101; Mismatches 249; Indels 212; Gaps 32;  
QY 22 SYOLGKHHMGSATKD-NQIAYIDDSKGAAPKTKNTMDQISAEGISAEQIVKITTQD 80  
Db 2 SYELGRHQAGQVKESNRVSYIDGDQAGQKA--ENLTPDEVSKREGINAQXVIKITDQG 59

[illegible]

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. RESULT 2
US-08-961-083-56
; Sequence 56, Application US/08961083
; Patent No. 6159469
;
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
;
; NUMBER OF SEQUENCES: 452
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
;
; ZIP: 20850
;

```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 796 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-961-083-56

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Query Match	21.7%	Score 949	DB 4	Length 796
Best Local Similarity	29.5%	Pred. No. 1.1e-68		
Matches 277	Conservative 100	Mismatches 214	Indels 348	Gaps 34
QY	22	SYOLOGHHMGSATKDNQIAYIDDSKGAKAPKT-NKTMQISAEGISAEQIVKITYDQG	80	
Db	1	SYELGLYQARTVKENNRVSYID--GKQATQKTENLTTPDEVSKREGINAEQIVIKITYDQG	57	
QY	81	YVTSHGDIHYFYNGKVPYDAIISELLMTDPNRYFKQSDVINETILDGVYIKNGNYYVYL	140	
Db	58	YVTSHGDIHYFYNGKVPYDAIISELLMKDPNYKLKDEDIVNEVKGGVYIKVDGKYVYL	117	
QY	141	KPGSKRKNIIRTKQOIAEQVAKGTKEAKEKGLAOVAHLKSEVAAVNEAKRQGRYTTDDGY	200	
Db	118	KDAHADNVRTKEEINRQKEHSQH-REGG-----TPRNDGAVALARSGRYTTDDGY	169	
QY	201	TFSPPTDIDDLGDAYLVPHGNHYHYPKKDLSPSELAAQAQVWSQKQGRG--ARPSDYRP	258	
Db	170	IFNADTIETDGIYIVPHGDHYHYPKNELASASELAAEAFLS--GRGLNSNRTYRR	226	
QY	259	TPAPAPGRKKAPIPDVTPNPGQGHODNGGYHPAPRRPNDASQNKHORDFEKGTKFELL	318	
Db	227	QNSDNTSRTNW-VPSVS-NPGTNTNTSN-----NSNTNSQAQSQND-----IDSL	271	
QY	319	DQLRLDLKYRHYEEDGLIFEPTQVYKSNAGFYVVPHGDIHIIIPRSQSLPLEMELAD--	376	
Db	272	KQLYKPLSQRHVESDGLVFDPAQITSTRTARGAVAVPHGDHYHFIFYQSOMSELEERARI	331	
QY	377	--RYLAGQTEDD-----DSGSD-----	391	
Db	332	PLRYRSNHWPDSRPEQSPQPTPEPSGPQAPAPNLKIDSNSLSVQLVRKVGEGYFEE	391	
QY	392	-----HSPSPDKE-VTHTFLGHR-----IKAY-----	412	
Db	392	KGISRYVEAKDLPSETVKNLSEKLSQESVSHLLTAKKENVAPRDQERYDKAYNLLTEAH	451	
QY	413	-----GKGLD-----GKP-----	420	
Db	452	KALFXNKGNSDFQALDLKLLERLNDESTNKEKLVDDLLAFLAPITHEERLQKPNQIEYT	511	
QY	421	-----YDTSDAYVESKESISHSYDKSGVTAKHGDHFHYIGFGELEQYELDEVAN	468	
Db	512	EDEVRIADLADKYTTSQYIFDEHDIISDEGDAYVTPRMGSHHWIGKDSLSDEKEKVAQA	571	
QY	469	WVKAKG-----QADELAAALDQEQGKEK-PLFDTKKVSRRVTKDKGKVGYYM	513	

```

Db      572  YTKKGI LPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLV-----RLEPMV 618
QY      514  PKDGKDYFYARDQLDLTQIAFAEQELMLKDKKHRYRDIYDTGIEPRLAVDVSSLEPMHAGN 573
Db      619  -----EH-----TVEVKN-----GN 628
QY      574  ATYDTGSSFEVPIHDIHVPRYSWL-----TRQIATIKYVMQHPVVRP---D 618
Db      629  -----LIIHKDHYHNKIFAWFDDHTYKAPNGYTLDELFATIKIYVEHPDERHSND 680
QY      619  IWSKPGHEESSVIYPNVTPLDKRAGMNPWQIIHSAEYVQKALAEGRFATPDGYLFDPRDV 678
Db      681  GW-----GNASEHYLGKKDHSEDPNKNFKADEEPVEETPAE---PE----- 718
QY      679  LAKETFWWKDGSFISIPRADGSSLRTINKSDLSQAEWQOAOELLAKKN---AGDATDT-- 732
Db      719  -----VPQVE-----TEKVEAQLKEAEVLLAKVTDSSILKANATETTLA 755
QY      733  -----DKPKEKQOQADK---SNENQOPSEASKEE 757
Db      756  GLRNNLTLOIMDNNSIMAEAEKLLALLKGSNPSSVSKEK 794

```

### RESULT 3

```

: Sequence 182, Application US/08361083
: Patent No. 6159469
:
: GENERAL INFORMATION:
: APPLICANT: Choi et. al.
: TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
: NUMBER OF SEQUENCES: 452
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Human Genome Sciences, Inc.
: STREET: 9410 Key West Avenue
: CITY: Rockville
: STATE: Maryland
: COUNTRY: USA
: ZIP: 20850
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
: COMPUTER: HP Vectra 486/33
: OPERATING SYSTEM: MSDOS version 6.2
: SOFTWARE: ASCII Text
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/961,083
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Brookes, A. Anders
: REGISTRATION NUMBER: 36,373
: REFERENCE/DOCKET NUMBER: PB340P2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (301) 309-8504
: TELEFAX: (301) 309-8512
: INFORMATION FOR SEQ ID NO: 182:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 447 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
: US-961-083-182

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	Query Match	19.28;	Score 839;	DB 4;	Length 447;	
	Best Local Similarity	39.98;	Pred. No. 4.1e-60;			
	Matches 178;	Conservative 65;	Mismatches 119;	Indels 84;	Gaps 10;	
OY	25 LKHHMGSATKDNOIAYIDDSKGAKAPKTNTKMDQISAEEGISAEQIVVKITDQGYYTS	84				
	:   :	:   :	:   :	:   :	:   :	:   :

[illegible]

## RESULT 4

```

: Sequence 4, Application US/08790912
: Patent No. 5976542
:
: GENERAL INFORMATION:
: APPLICANT: Weiser, Jeffrey N.
: APPLICANT: Plaut, Andrew G.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
: TITLE OF INVENTION: OF STREPTOCOCCUS PNEUMONIAE INFECTION
: NUMBER OF SEQUENCES: 10
:
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
: STREET: 1601 Market Street, 36th Floor
: City: Philadelphia
: STATE: Pennsylvania
: COUNTRY: USA
: ZIP: 19103-2398
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/790,912
: FILING DATE: 29-JAN-1997
:
: CLASSIFICATION: 424
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/026,939
: FILING DATE: 23-SEP-1996
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Leary, Kathryn
: REGISTRATION NUMBER: 36,317
: REFERENCE/DOCKET NUMBER: 7600-4U1
:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 567-2020
: TELEFAX: (215) 567-2991
:
: TELEX: 831-494
:
: INFORMATION FOR SEQ ID NO: 4:
:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1861 amino acids
: TYPE: amino acid
: STRANDEDNESS:
:

```





Db 273 ---DVEEKL EETGYGFREREFTTRILVKKRRNKEQKKLEKEDKEKKLIAAEPDDEKKIKL 329

QY 327 KYRHYEEDGLIFEPTQVIXN-AFGYVVPBGHDYHIIPRSQLSPL---EMELADRYLAG 381

Db 330 K-----DSDDKVVPVNNKNSFPDKFRAPDKKRTMYRLSELPIVPRKDNELA---VCG 382

QY 382 QTEDDSGSDHSPSKDEVTHTF-----LGHRIKAYGKGL----- 416

Db 383 DSM-----SKVNGKKLKSTFNPKRRRNKLKERKMQELHKKKNYKKYKLLEREKR 435

QY 417 ---DGKPYDTSDAYVFSKESHSVDKSGVTAKHGDPHYIGFGELEQYELDEVANWVK-- 471

Db 436 ENPDGEPLNTPRIHVIRPSDL--MDK-GENKSAGHPFKYQPTKGLKEYEESHVSKDYOLE 492

QY 472 -----AKGQADELAALDQEQKEKPLFDTKKVSRKVTKDGVGYMMPKDKDYF 521

Db 493 HEPPTKLPEYKGVHSR-EYQLDHEPPTKLPEYKGVHSREYQLDNEVRDELPEYKGVH 551

QY 522 YARDQLD---LTQIAFAEQELML-KDKKHRYDIYDTGIEPRLA--VDYSSLPMHAGNA 574

Db 552 SREYQLDNEGSPSTLKEQDTELAKGKDTINKPHESVDEYDQTELAKGKDTINKP-HESVD 610

QY 575 TYDTGSSFVIPHIDHIVVPYSWLTRDQIATIKYVMOHPVPRD-----IWSK 622

Db 611 EYD-----QSELAKGKDTINKPHESVDEYDQTELAKGKEVTNK 648

QY 623 PGHEESGVIPNVTPLDKRAGMPNWOIHSAEVQKALAEGRFAT-----PDGYIFDPR 676

Db 649 P-HENLEEY--NETDLAKGKEVTNKPHESVDEYDQSELAKGKDTINKPHESVDEY--DQ 702

QY 677 DYLAKETFWKDGSSIPRADGSSLRITINKSDLSQAEWQAOELL--AKNAGDATDTDK 734

Db 703 TELAK-----GKEVTNKARENLEEYNETDLA-----KGKEVTNKARENLEEYNETDL 749

QY 735 PKEQOADSNNQOPSEASKEEKESD 762

Db 750 AKGKEVTNKAHEN-----LEEYNETD 770

RESULT 6

PCT-US93-07261-16

Sequence 16, Application PC/TUS9307261

GENERAL INFORMATION:

TITLE OF INVENTION: PFEMP3 MALARIA ANTIGEN, ANALOGS, ANTIBODIES AND USES THEREOF

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: John H. C. Blasdale

STREET: One Giralda Farms

CITY: Madison

STATE: New Jersey

COUNTRY: USA

ZIP: 07940-1000

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 6.0.5

SOFTWARE: Microsoft Word 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/07261

FILING DATE: 19930805

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/927,531

FILING DATE: 07-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: Blasdale, John H. C.

REGISTRATION NUMBER: 31,895

REFERENCE/DOCKET NUMBER: DX0288K

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-822-7398

TELEFAX: 201-822-7039

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 1663 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Plasmodium falciparum

STRAIN: Malayan Camp

PCT-US93-07261-16

Query Match 3.3%; Score 142.5; DB 5; Length 1663;

Best Local Similarity 20.0%; Pred. No. 0.015;

Matches 174; Conservative 120; Mismatches 341; Indels 233; Gaps 38;

QY 27 KHHMSATRDNOIAYIDSKGKAAAPKTN-----KTMQISAEEGISAEQIYVKTDOGY 81

Db 4 KEALKQKTEKNEKARNALKEKKLEKQKKNDQAQAKDLTKRESQDSSSEKSLKEKVGEL 63

QY 82 VTSBGDHYHFNKVPYDAIISELLMTDPNRYRFKQSDVINEILDG--YVIKVGNG---- 135

Db 64 KEKE-----NKETLKKKELENQKEKEKNKIKDNNDALKNKGNDKD 106

QY 136 -YVYVYLKPGSKRRNIR---TKQIAEQVAKGTKEAKEK-----GLAQVA 175

Db 107 KKITVPKKRESVEKDKEMELKEKEFIKQHLKDYEEKKEKRRNWILSLRDKLREIQLE 166

QY 176 HLSKEEVAAVNEAK-----ROGRYTTDDGYIFSPD-----IDDL 211

Db 167 KLNAQLESALINELKERRASRRPMVMKQGMKDEVDEWIKKYDDEQAEEKNGTKDEITKD 226

QY 212 GDAY--LVP---HGNHYHYPKDLSPSELAAQAYWSQKQGRGARPSPDYRPTPAPAPGR 266

Db 227 GDGYEEIETKFGYGMRENALGELD-EYEEYKERYIKEDGEG---DLK----- 272

QY 267 RKAPIDVTPNPGQGHQPDNGYHPAPRPNDASQNHQORDEFKGTFKELDLQHLRLDL 326

Db 273 ---DVEEKL EETGYGFREREFTTRILVKKRRNKEQKKLEKEDKEKKLIAAEPDDEKKIKL 329

QY 327 KYRHYEEDGLIFEPTQVIXN-AFGYVVPBGHDYHIIPRSQLSPL---EMELADRYLAG 381

Db 330 K-----DSDDKVVPVNNKNSFPDKFRAPDKKRTMYRLSELPIVPRKDNELA---VCG 382

QY 382 QTEDDSGSDHSPSKDEVTHTF-----LGHRIKAYGKGL----- 416

Db 383 DSM-----SKVNGKKLKSTFNPKRRRNKLKERKMQELHKKKNYKKYKLLEREKR 435

QY 417 ---DGKPYDTSDAYVFSKESHSVDKSGVTAKHGDPHYIGFGELEQYELDEVANWVK-- 471

Db 436 ENPDGEPLNTPRIHVIRPSDL--MDK-GENKSAGHPFKYQPTKGLKEYEESHVSKDYOLE 492

QY 472 -----AKGQADELAALDQEQKEKPLFDTKKVSRKVTKDGVGYMMPKDKDYF 521

Db 493 HEPPTKLPEYKGVHSR-EYQLDHEPPTKLPEYKGVHSREYQLDNEVRDELPEYKGVH 551

QY 522 YARDQLD---LTQIAFAEQELML-KDKKHRYDIYDTGIEPRLA--VDYSSLPMHAGNA 574

Db 552 SREYQLDNEGSPSTLKEQDTELAKGKDTINKPHESVDEYDQTELAKGKDTINKP-HESVD 610

QY 575 TYDTGSSFVIPHIDHIVVPYSWLTRDQIATIKYVMOHPVPRD-----IWSK 622

Db 611 EYD-----QSELAKGKDTINKPHESVDEYDQTELAKGKEVTNK 648

QY 623 PGHEESGVIPNVTPLDKRAGMPNWOIHSAEVQKALAEGRFAT-----PDGYIFDPR 676

Db 649 P-HENLEEY--NETDLAKGKEVTNKPHESVDEYDQSELAKGKDTINKPHESVDEY--DQ 702

QY 677 DYLAKETFWKDGSSIPRADGSSLRITINKSDLSQAEWQAOELL--AKNAGDATDTDK 734

Db 703 TELAK-----GKEVTNKARENLEEYNETDLA-----KGKEVTNKARENLEEYNETDL 749

QY 735 PKEQOADSNNQOPSEASKEEKESD 762

Db 750 AKGKEVTNKAHEN-----LEEYNETD 770



```
RESULT 7
US-08-596-291-3
; Sequence 3, Application US/08596291
; Patent No. 5821075
; GENERAL INFORMATION:
; APPLICANT: GONEZ, LEONEL JORGE
; APPLICANT: SARAS, JAN
; APPLICANT: CLAESSON-WELSH, LENA
; APPLICANT: HELDIN, CARL-HENRIK
; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/596,291
; FILING DATE: 09-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/115,573
; FILING DATE: 01-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: L0461/7000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; TELEX: 92-1742 EZEKTEL
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2465 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-596-291-3

Query Match          3.0%; Score 133; DB 2; Length 2465;
Best Local Similarity 19.9%; Pred. No. 0.16;
Matches 176; Conservative 114; Mismatches 322; Indels 272; Gaps 44;

QY 9 GSVAAILLATHIGSYOLGKHHM--GSATKDNQIAYIDDSKGAKAPKTNTMD-QISAE 64
DB 1422 GQVYVHLLLEK--GQSPTSKEHVPTPQCTLSDNA---QGQPEKVKKTQYKDYSFVTE 1476
QY 65 EGISAEQIVVKITDQGYVTSBGDHYHFYNGKVPYDAIISEELMTDPNRYRKQSDVINEI 124
DB 1477 ENTFEVKLFKNSSGLGFSPRED--NLIPEQINASTIVRVKLFAGQPAESCKIDVGDI 1534
QY 125 LDGYVIKNGNYVYVLKPGSKRNIRT-----KQQ 154
DB 1535 L-----KVNG---ASLKGLSQOEVIASLRGTAPEVFLLCRPPGVLPEIDTALLPLQS 1586
QY 155 IAEQYAKGTKEAKEKGLAQAVALSKKEVAAVNEAK-----RQGRYTT-----DDGYIFS 203
DB 1587 PAQVLPNSSKDSQSPSCVEGTSISDENEMSDSKKQCKSPSRDSYSDSSSGEDDLVTA 1646
QY 204 PTDTIDDLGDAYL-----VFHGNHYHYIPKKDLSPSELAAQAYWSQKQGRGARPSDY 256
DB 1647 PANISNTWSSALHQTLSNMYSOAQOSHHAEPK---SQEDTICTMFTYYPQKIPNKEFEEDS 1703
QY 257 RPTPAPAPGRKKAPIPDVTPNPGQGHQPDNGGYHPAPRPNDASQNKHQRDEFKCKTFKE 316
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DB 1704 NPSPLP-----PDMA--PGQSYQPQS-----ESASSSSMKYHIHISEPTROE 1745
QY 317 LLDQLHRLDLKYRYHVEDGLIFE-PTQVIKSN--AFGYVPHGDHIIIPRSQSPLEME 373
DB 1746 NWTPPL-KNDLE-NHLEDELEVELELLITLIKSEKASLGFTVTGN-----Q 1788
QY 374 LADRYLAGQTEDDDSGSDHSPKPSDK-----EVTHTFLGHRKAYGKG---LDGK 419
DB 1789 RIGCYVHDVIQDPKSPDGRKLPQDRLIKVNPDVTNMTHTDAVNLLRAASKTVRLVIGRV 1848
QY 420 PYDTSDAYVESKESHSYVDKSGVTAKHGDHFHYIGFGELOYELDEVANMWKAKGADEL 479
DB 1849 PRITQNTNVASFATGH-----KLTCKNKEEL 1873
QY 480 AALDQEQKEKPLPDTKKVSRKVTKDGVGYMMKDKDYFYARDQDLDTQIAFAEOEL 539
DB 1874 GFSL---CGHDSLYQVYIIS-----DINRSVAALIEGNL 1905
QY 540 MLKDKKHRYDIVDTGT---EPRLAVDVSSSLPMHAGNATYDTGSSFVIPHIDHIVPYS 596
DB 1906 QLDVIHYVNGVSTQGMTEEVNRALDM-SLPSLVLKATR-----NDLPVVPSS 1953
QY 597 WLTRDQIATIKYVMQHPPEVRPDIWSKPGHEESGVT-PNVTPLDKRAGMNPQIISAE 655
DB 1954 --KRSVSA-----PKSTKNGSYSVSGSQPALTPNDSFSIV-----AGEE 1993
QY 656 VQK-ALAEGRFATPDGYIF--DPRDLAKETFWKDGFSIPRADGSSLRTINKSDLSQA 712
DB 1994 INEISYPRKGCST--YQIKGSPNLTLPKESYIQEDDIY-----DDQEAEVYQSLDV 2045
QY 713 EWOQAQELLAKKN-AGDA-----TDTD---KPREKQADKSN-----745
DB 2046 D-EEAQNDLNNNAAGDSGCPGLKMGKLSERTEDTDCDGSPLPEYFTEATKMGCEE 2104
QY 746 --ENOQPSSEA--SKEEKESDD-----FIDSLPDYGLDRATLED 780
DB 2105 YCEEKVKSESLIQPKQEKKTDDDEITWGNDELP--IERTNHED 2145
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RESULT 8
US-09-100-804-3
; Sequence 3, Application US/09100804
; Patent No. 6066472
; GENERAL INFORMATION:
; APPLICANT: GONEZ, LEONEL JORGE
; APPLICANT: SARAS, JAN
; APPLICANT: CLAESSON-WELSH, LENA
; APPLICANT: HELDIN, CARL-HENRIK
; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,804
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/596,291
; FILING DATE: 09-AUG-1996
; APPLICATION NUMBER: US 08/115,573
```

FILING DATE: 01-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/09943  
FILING DATE: 01-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: GATES, EDWARD R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/DOCKET NUMBER: LO461/7003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2465 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-100-804-3

Query Match 3.0%; Score 133; DB 3; Length 2465;  
Best Local Similarity 19.9%; Pred. No. 0.16;  
Matches 176; Conservative 114; Mismatches 322; Indels 272; Gaps 44;

QY 9 GSAAILLATHIGSYLGKHHM--GSATKDNQIAYIDDSKGRKAKAPKTNKTM--QISAE 64  
DB 1422 GQVHLLLEK--GQSPTSKEHVPTPQCTLSQNA---QGQPEKVKTTQVKDYSEVTE 1476  
QY 65 EGISAQIVKRTDQGYVTSBGHDHVFNGKVPYDAIIESELLMTDPNRYFKQSDVINEI 124  
DB 1477 ENTFEVKLEKNSGGLGFSFSRED--NLIEQINASIVRVKLLRAGOPAAESGKIDVGDI 1534  
QY 125 LDGYIVKNGNYYVYLKPGSKRKNIRT-----KQ 154  
DB 1535 L-----KVNQ--ASLKLGSQEVISALRGTAPEVFLLCRPPGVLPEDTALLTPLQS 1586  
QY 155 IAEQVAKGTRKAKEKGLAQVAHLKSEVAAVNEAK-----RQGRYTT-----DDGYIFS 203  
DB 1587 PAQVLPNNSKDSQSPSCVEQSTSDENEMSDSKKQCKSPSRDSYSDSSGSGEDDLVTA 1646  
QY 204 PTDIIDLDGDAYL-----VPHGNHYIYIPKDLSPSELAAQAYWSQKQGRGARPSDY 256  
DB 1647 PANISNSTWSSALHQTLSNMVSAQASHNEAPK--SQEDTICMIFYYPQKIPNKPFEEDS 1703  
QY 257 RPTPARAPGRKAPRPDVTNPNQGGHQRPDNGGYHAPRRPNNDASQNKHQRDEFKGTKE 316  
DB 1704 NPSPLP-----PDMA--PGQSYQPOS-----ESASSSSMDKYHHIHISEPTROE 1745  
QY 317 LLDQLHRLDLKYRHEVEDGLIFE-PTQVIXSN--AFGYVPHGHDHYHIIPRSQSPLEME 373  
DB 1746 NWTPL-KNDLE-NHLEDFELEVELLITLIKSEKASLGFTYTKN-----Q 1788  
QY 374 LADRYLAGOTEDDDSGSDHSPSK-----EVTHFFLGHRIKAYGK-----LDGK 419  
DB 1789 RIGCYVHDVYIQPAKSDGRLKPGDRLLIKVNDTDTNMTHTDAVNLLRAASKTVRLVIGRV 1848  
QY 420 PYDTSADVFSKESIHVSVDKSGVTAKHGDHFHYIGFGELEQYELDEVANWVKAKQADEL 479  
DB 1849 PRITQNTNVAASFATGH-----KLTCKNEEL 1873  
QY 480 AALDQEQEKERPLFDTKKVSRYTKDGKVGYPMPKDKDYFYARDQLDLQIAFAQEL 539  
DB 1874 GFSL---CGGHSLSLYQVYIS-----DINPRVAIEGNL 1905  
QY 540 MLKDKKHRYVDIVDTGI---EPRLADVSSLPMHAGNATYDTGSSFVIPHIDHIVVPS 596  
DB 1906 QLLDVHYVNGVSTQGMTELEVNRALDM-SLPSLVLKATR-----NDLPPVPS 1953  
QY 597 WLTRDQIATIKYVMQHPVRPDIWSKPGHEESGVI-PNVYPLDKRAGMPNWQIHSAAE 655  
DB 1954 --KRSAYSA-----PKSTKNGSYSGSCSQPALTPNDSFSTV-----AGEE 1993  
QY 656 VQK-ALAEGRFATPDGYIF--DPRDYLAKETFWWKDGSFIPRADGSSSLRTINKSDLSQA 712

DB 1994 INETSYPKGCST---YQIKGSPNLTLPKESYIQEDDIY-----DSDQAEAVIOSLLDV 2045  
QY 713 EMQAOELLAKN-AGDA-----TDTD--KPKKQQAADKSN----- 745  
DB 2046 D-EEQONLLNENNAAGDSGCGPTLKMNGKLSERTEDTDCDGSPLPEYFTEATKMGCEE 2104  
QY 746 --ENQOPSEA--SKEEKESDD-----FIDSLPDYGLDRATLED 780  
DB 2105 YCEEKVKSSESLIQPKQEKTTDDEITWGNDELFP--IERTNHED 2145

RESULT 9

US-08-296-791-3  
Sequence 3, Application US/08296791  
Patent No. 6245337

GENERAL INFORMATION:

APPLICANT: St. Gene III, Joseph W.  
APPLICANT: Falkow, Stanley  
TITLE OF INVENTION: Haemophilus Adherence and Penetration  
TITLE OF INVENTION: Protein  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/296,791  
FILING DATE: 25-AUG-1994  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-59941/RFT/RMS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1541 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
US-08-296-791-3

Query Match 3.0%; Score 131.5; DB 4; Length 1541;  
Best Local Similarity 17.5%; Pred. No. 0.1;  
Matches 153; Conservative 111; Mismatches 294; Indels 315; Gaps 37;

QY 44 DSKGAKA-----PKTNKTMQDISAEQISAEQIVKTTDQGYVTSBGHDHYHFNKG 95  
DB 462 DNKSLKVGDTVILKQQTNGSGQHAFASVIGRSTLVLLNDKQVDPNSIYFGFRGR 521  
QY 96 -----VPYDAI-----ISELLMTDPN-----YRFKQSDVIN- 122  
DB 522 LDNGNSLTFDHNRIDDGARLVNHNMTNANITITGESLITDPNITTPRYNIDAPDEDNP 581  
QY 123 ---EILDG---YVIKNGNYYVYLKPGSKRKNI-----RTKQIAEQVA 160  
DB 582 YAFRIKIDGGQLYLNLNENYTYALRKGASTRSELPPKNGSESNENMLYMGKTSDEAKRNV 641  
QY 161 K-----GTRKAKEKGLAQVAHLKSEVAAVNEAKRQGRYTTDDGYIFSPTD 206  
DB 642 NHINNERMNGENGYGEEEGKNNGNLNVTFKKGSE-----QNRFLLTG-----TN 687



QY 740 -----QADKSNENQPPSEASKKEESDDFIDS 767  
Db 1137 ETVQPAEPAREN-DPTVNIKEPQSGTNTTADT 1168

## RESULT 11

US-09-514-302-4  
; Sequence 4, Application US/09514302  
; Patent No. 6338959  
; GENERAL INFORMATION:  
; APPLICANT: HATADA, Yuji  
; APPLICANT: IGARASHI, Kazuaki  
; APPLICANT: OZAKI, Katsuya  
; APPLICANT: ARA, Katsutoshi  
; APPLICANT: KAWAI, Shuji  
; APPLICANT: ITO, Susumu  
; TITLE OF INVENTION: GENE FOR ENZYME HAVING BOTH ALKALINE PULLULANASE AND  
; TITLE OF INVENTION: ALKALINE ALPHA-AMYLASE ACTIVITIES  
; FILE REFERENCE: 2173-105P  
; CURRENT APPLICATION NUMBER: US/09/514, 302  
; EARLIER FILING DATE: 2000-02-28  
; EARLIER APPLICATION NUMBER: 08/952, 084  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 893  
; TYPE: PRT  
; ORGANISM: Bacillus sp.  
US-09-514-302-4

Query Match 2.9%; Score 129; DB 4; Length 893;  
Best Local Similarity 18.7%; Pred. No. 0.071;  
Matches 131; Conservative 74; Mismatches 218; Indels 276; Gaps 33;

QY 1 VKKTYGIGSVAAILLATHIGSYQLGKHHMSAT-----KDNQIAYIDDSKGAKAPK 53  
Db 90 IDEMYAYDGKLGAE-----HEDGTATLKVSPKADNVSVLVD---KVDQNE 134  
QY 54 TNKTMDOISAEEGISAEOIVKIT--DQGYVTSBGDHYHFYNGKVPYDAIISELLMTDP 111  
Db 135 VVDTEIEMVKGRGWS---VKLTGDNGLDLSKGYHH----- 169  
QY 112 NYRFKQSDVINELDGYVIKNGNYVYLKPGSKRKNIRTKQOIAEOVAKGTKEAKE-- 169  
Db 170 -YEITHGDTVNLALDPY-----AKSMAAWNNEAGDKVG 201  
QY 170 --GLAQVAHLSKEEVAANEAKRGRYTTDDGYIFS--PTDIIDD--LGDAYLVPHGNHY 223  
Db 202 KAAIVDIGSIGPE---LDYADIPGFEKREDTIIYEVHVRDFTSDPNIGEDLKAQFGTFA 257  
QY 224 HYIPKCDLSPSELAAQA-----YWSQKQGRGAPSDYRPTAPAPGRKRAPIDVT 275  
Db 258 SFVEKLDYI-QELGVTHIQLLPVMSTYFSNEFESGERMLEYASTGT----- 302  
QY 276 PNPQGHQPDN-----GGYHPAPRPNDASQNKHQRDEFGKTEKELLQDLHR-----L 324  
Db 303 -NYNWGYDPHNYFSLSGMYSNPEDP-----ELRIKEFKNLINIEIHKRDMGVVL 350  
QY 325 DLKRYHVEEDGLIFEPTQVYKSNAGFYVPHGDHYHIIPRSQLSPLEMELADRYLAGQTE 384  
Db 351 DVVFNHTAQ-----VHIFEDLVP--NYHHFM----- 374  
QY 385 DDDSGSDHSPSKDEKVTHTFLGHRKAYGKGLDGKPYDTSDAYVFSKESI--HSVDKSGVT 443  
Db 375 -DADGTPRT-----SFGGRLGTTHEMSRRLV--DSIKHWVDEYKV- 413  
QY 444 AKHGDHFHYIGFELE--QYELDEV-----ANWYKAKQADELAALDQE----- 486  
Db 414 --DGFREFMDMGDHADESIGIAFDEAKKLNPNIVMIGEGWYTFAGDEGEPPVADQQWMOY 471  
QY 487 -----QGKEKPLEDTKKVSRKVTKDGKGYMMPKDG-----KDYFARDQDLDTQ 531

Db 472 TEAVGSFSEDFRNLKSGFSGEGQPRFIT--GGAENVQOIFDNIIKAQPHNEMADQPGDVVO 530  
QY 532 IAFAEQELMLKDKKHYRIDVIDTGIEPRLAVDVSSLPMA---AGNA----- 574  
Db 531 YIEAHDNLT-----YDVIAQSIKKDPEIAENDEIHKRIRVGNAMVLTSGTAFLLHA 583  
QY 575 -----TYDT---GSSFYIPIHDH 589  
Db 584 GQEFFRTKQWRAPATEAPYKSTYMTDADGNPFVYPYFIH 622

## RESULT 12

US-09-514-302-2  
; Sequence 2, Application US/09514302  
; Patent No. 6338959  
; GENERAL INFORMATION:  
; APPLICANT: HATADA, Yuji  
; APPLICANT: IGARASHI, Kazuaki  
; APPLICANT: OZAKI, Katsuya  
; APPLICANT: ARA, Katsutoshi  
; APPLICANT: KAWAI, Shuji  
; APPLICANT: ITO, Susumu  
; TITLE OF INVENTION: GENE FOR ENZYME HAVING BOTH ALKALINE PULLULANASE AND  
; TITLE OF INVENTION: ALKALINE ALPHA-AMYLASE ACTIVITIES  
; FILE REFERENCE: 2173-105P  
; CURRENT APPLICATION NUMBER: US/09/514, 302  
; EARLIER FILING DATE: 2000-02-28  
; EARLIER APPLICATION NUMBER: 08/952, 084  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1938  
; TYPE: PRT  
; ORGANISM: Bacillus sp.  
US-09-514-302-2

Query Match 2.9%; Score 129; DB 4; Length 1938;  
Best Local Similarity 18.7%; Pred. No. 0.23;  
Matches 131; Conservative 74; Mismatches 218; Indels 276; Gaps 33;

QY 1 VKKTYGIGSVAAILLATHIGSYQLGKHHMSAT-----KDNQIAYIDDSKGAKAPK 53  
Db 1135 IDEMYAYDGKLGAE-----HEDGTATLKVSPKADNVSVLVD---KVDQNE 1179  
QY 54 TNKTMDOISAEEGISAEOIVKIT--DQGYVTSBGDHYHFYNGKVPYDAIISELLMTDP 111  
Db 1180 VVDTEIEMVKGRGWS---VKLTGDNGLDLSKGYHH----- 1214  
QY 112 NYRFKQSDVINELDGYVIKNGNYVYLKPGSKRKNIRTKQOIAEOVAKGTKEAKE-- 169  
Db 1215 -YEITHGDTVNLALDPY-----AKSMAAWNNEAGDKVG 1246  
QY 170 --GLAQVAHLSKEEVAANEAKRGRYTTDDGYIFS--PTDIIDD--LGDAYLVPHGNHY 223  
Db 1247 KAAIVDIGSIGPE---LDYADIPGFEKREDTIIYEVHVRDFTSDPNIGEDLKAQFGTFA 1302  
QY 224 HYIPKCDLSPSELAAQA-----YWSQKQGRGAPSDYRPTAPAPGRKRAPIDVT 275  
Db 1303 SFVEKLDYI-QELGVTHIQLLPVMSTYFSNEFESGERMLEYASTGT----- 1347  
QY 276 PNPQGHQPDN-----GGYHPAPRPNDASQNKHQRDEFGKTEKELLQDLHR-----L 324  
Db 1348 -NYNWGYDPHNYFSLSGMYSNPEDP-----ELRIKEFKNLINIEIHKRDMGVVL 1395  
QY 325 DLKRYHVEEDGLIFEPTQVYKSNAGFYVPHGDHYHIIPRSQLSPLEMELADRYLAGQTE 384  
Db 1396 DVVFNHTAQ-----VHIFEDLVP--NYHHFM----- 1419  
QY 385 DDDSGSDHSPSKDEKVTHTFLGHRKAYGKGLDGKPYDTSDAYVFSKESI--HSVDKSGVT 443  
Db 1420 -DADGTPRT-----SFGGRLGTTHEMSRRLV--DSIKHWVDEYKV- 1458





TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1076 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-074-658-19

Query Match 2.9%; Score 128.5; DB 4; Length 1076;  
Best Local Similarity 20.1%; Pred. No. 0.1;  
Matches 141; Conservative 87; Mismatches 244; Indels 231; Gaps 40;

QY 3 KTYGIGSVAAILLATHIGSYQLK----HHMSATKDNQIAYI---DD--SKGK---- 48  
DB 148 KNYAAGGAINIEIY-ENVRSEIISKANSSEYSGALSGVAFTKTADDIICKDKMGV 206  
QY 49 ----AKAPKNTKMDQISAEIGISAEQIVKTD--QGYVTHSGDHYHFYNGKVPYDAI 101  
DB 207 QTKTAYASKNNAWVNSVAAAGKAGSFGSLIYTDREGQY-KAHDD--AYQGSQSFDR 262  
QY 102 ISEELMTDPNRYFKOSDVINEILDGYIVKNGNYVYLKPG-----SKRKNIPTKQIA 156  
DB 263 VA---TTDPNNR--TFLIANEC-----ANGNYEACAGGQTKLQAKPTNVRDKVNYK 309  
QY 157 EQVAKG-----TKEAKEKGLAQVAHLS-KEEVAAVNEAKRGQRYTTDDGYIFSPDII 208  
DB 310 DYTGPNRLLIPNLTQDSKSLLRPGYQLNDKHVYGVEYETKQ-NYAMQDKTV----- 361  
QY 209 DDLGDALVPHGNHYHIYPKKDLSPSEL---AAQAQYWSQKRGARPSDYRPTPARPG 265  
DB 362 ---PAVLAVH-----DIEKSRLSNHAQANGY-OGNNLGERIRD----- 396  
QY 266 RRAKPIPDVTPNPGQHQPNDNGYHAPRRPNDASQNKHQDEF-----KGTPEK 315  
DB 397 -----TIGPDSGYINAHGVFY-----DEKHQKDLGLEVYVYDSKGEMKWF 439  
QY 316 ELLDQLHLRLD-----KYRHEEDGL--IPEPTQVYIKSNAFGYVVPH----- 355  
DB 440 DVRSYIDKQDITLRSQLTNTHGSHYPHIDKNTCPDVNKPFSVKEVDNNAYKEQHNLKAV 499  
QY 356 -----GDHYHIIPR-----SOLSPLEMLADRYLAGQTEDDSDGSHKPSDEY 400  
DB 500 FNKKMALGSTHHINLQVGYDKFNSSLSRVEYRLA-----THQSYQLDYTPPSNP-- 550  
QY 401 THTEIGHRIKAYGKGLDKPYDTSDAYVFSKESIHSVDSKSGVTAKHGDHFHYIGFELLEQ 460  
DB 551 ---LPDKFKPI-LGSNNKPI-CLDAYGYGHD-----HPQACNAKNSTYQNFALIKGIEQ 599  
QY 461 YELDEVANWVAKAQADEL---AALDQ--EQGKEKPLFDTKKVS-----KYTKDGKVG 511  
DB 600 Y-----NOKTNTDKIDYQAIIDQYDKQNPNSITLKPEFIKQSLGQEKYKIDELGF 650  
QY 512 MMRKD-----GKDYFYARDQLDLTQIAFAEQELMLKDKKHRYDIV 552  
DB 651 KAYKDLRNEWAGWTNDNSQONANKGTDNITQ-----PNQATVVKDDK-CKYS-- 696  
QY 553 DTGIEPRLAVDVSSLPMHAGNATYDTGSSFVIPHIDHVVY 595  
DB 697 ---ETNSYADCSTTPRHI-----SGDNYFIALKDNMTINKY 729

RESULT 15  
US-08-663-112-2  
; Sequence 2, Application US/08663112  
; Patent No. 5849503  
; GENERAL INFORMATION:  
; APPLICANT: MAGATSUMA, Masako  
; APPLICANT: KURITA, NO. 5849503iko  
; TITLE OF INVENTION: MUTANT PROTEINS OF HUMAN DNA  
; TITLE OF INVENTION: TOPOISOMERASE I

NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner L.L.P.  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/663,112  
FILING DATE: 26-NOV-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Einaudi, Carolyn P.  
REGISTRATION NUMBER: 32,220  
REFERENCE/DOCKET NUMBER: 06609.1488-00000  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 765 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-663-112-2

Query Match 2.9%; Score 127; DB 2; Length 765;  
Best Local Similarity 20.1%; Pred. No. 0.082;  
Matches 137; Conservative 90; Mismatches 240; Indels 214; Gaps 34;

QY 141 KPGSKRKNIPTKQIAEQVAKGTKEAKEKGLAQVAHLSK-----EEVAAVNEAK 189  
DB 42 KDKREKSKHNSSEHDSKKHKEKEKTKHKKDSSSEKHKDKKDRDKREKKEKVRASGDAK 101  
QY 190 RQGRYTTDDGYIFSPDIIID-LGDALVPHGNHYHIYPKKDLSPSELAAQAQYWSQKQ 248  
DB 102 I--KKEKENGF--SSPQIKDEPEDDGYVP-----PKEDIKP-----LKR 139  
QY 249 RGARPSDYRPTPARAPGRKAPIPDV-TPNPGQHQPNDNGYHAPRRPNDASQNKHQ 307  
DB 140 RDEDDVDYKPKIKETEDTKKRRKLEBEDGKLKPKNKDKKRVPEPDNKKKPKKEE 199  
QY 308 EFKGTFKELLDLHLRLDKYRHEEDGLIPEPT-----QVIK----- 345  
DB 200 EQKWKWEE--ERYREGIKWKFLEHKGVPFAPRYEPLPENVKFYDGVKMLSPKAEV 256  
QY 346 SNAFGYVVPH-----GDHYHIIPRSQLSPLEMLADRYLAGQTE 384  
DB 257 ATFFAKMLDHEYTTEIFRKNFEDKWRKEMTNEKNII--TNLSKCDFTQMSQYFKAQTE 314  
QY 385 DDDSGSDHSKPSDKEVTHTEFLGHRKAYGKGLDKPYDTSDAYVFSKESI--HSVDSKV 442  
DB 315 ARKQMSKEEKLIKKEENKLL---KEVG-----FCIMDNH---KERIANFKIEPGL 360  
QY 443 TAKHGDHFHYIGFELLEQYELDE--VANWVAKAQADELAALDQEQGKEKPLFDTKVY 499  
DB 361 FRGRGNH--PKMGLKRRIMPEDIILNCSK-----DAKVPSPPGHKWKEVR 405  
QY 500 -SRKYT-----KDGKVGVM-----PKDGKDYFYARDQLDLTQIAFAEQELML 541  
DB 406 HDNKVTWLVSTENIQGSIKYIMLNSSRIKGEKDWQKYETAR-----RLKCV 455  
QY 542 KDKKHRYVDIVDTGIEPR---LAVDVSSLPMHAGN-----ATYDTGS--SFVIPHID-- 588  
DB 456 KIRNQYREDWKSKEMKVRQRAVALYFIDKLALRAGNEKEEGETADTVGCCSLRVEHNLH 515

Mon May 19 08:34:07 2003

us-09-645-835a-2.may19.ra

Page 12

```
QY      589 -----HIVVPSWLTRODIATIKIYMQHPEVRPDIWSKEGHEESGSVIPNVTPLDKRAG   643  
        :|| : || :|| :||  
Db      516 PELDGOEYVEFELGKD---SIRYY-----NKVYEKRV-   547  
  
QY      644 MPNWQIHSAEEVOKALAEGRFATPDGYIFDPRD--VLAKETFWWKDGFSFIPIRADGSSL   701  
        | |: :: | :|| : ||| . :|  
Db      548 FKNLQLFMENKQ-----PEDDLFDRLNTGITLNKHLDLMEG-----LTAKVF   589  
  
QY      702 RTINKSDLSQAEMOAOCELLA   722  
        || | | | || :|| |  
Db      590 RTFNASITLQ---QLKLKELTA   607
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Search completed: May 19, 2003, 08:24:40  
Job time : 27.8853 secs



GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2003, 07:51:03 ; Search time 12.3699 Seconds  
(without alignments)  
1883.841 Million cell updates/sec

Title: US-09-645-835A-4

Perfect score: 4080  
Sequence: 1 MKTKKVIILVGLLSQLT.....DHDHEHEDENAKDEQNHAD 792

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A-COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B-COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A-COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B-COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS-COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	322.5	7.9	746	5	PCT-US95-10509-2
2	233	5.7	447	4	US-08-961-083-182
3	223	5.5	796	4	US-08-961-083-56
4	204	5.0	763	4	US-08-961-083-66
5	174.5	4.3	947	4	US-09-228-986-73
6	168	4.1	708	4	US-09-131-648-2
7	167	4.1	1112	4	US-09-353-585-2
8	167	4.0	910	4	US-09-228-986-72
9	165	3.9	968	4	US-09-180-439-3
10	160	3.9	968	4	US-09-180-439-4
11	160	3.9	799	4	US-09-180-439-6
12	159	3.8	359	1	US-08-303-238-4
13	155.5	3.8	359	4	US-08-458-834-4
14	155.5	3.8	603	1	US-08-190-802A-50
15	153.5	3.8	603	4	US-08-477-346-50
16	153.5	3.8	603	4	US-08-473-089-50
17	153.5	3.8	603	4	US-08-473-089-50
18	153.5	3.7	605	1	US-08-190-802A-49
19	152.5	3.7	605	4	US-08-477-346-49
20	152.5	3.7	605	4	US-08-473-089-49
21	152.5	3.7	605	4	US-08-473-089-49
22	152.5	3.7	980	2	US-08-473-553A-6
23	152.5	3.7	985	2	US-08-473-553A-2
24	152.5	3.7	806	4	US-08-945-983-2
25	151	3.7	863	2	US-08-666-271-2
26	151	3.7	353	6	5340934-4
27	150.5	3.7			Patent No. 5340934

28	150	3.7	1016	4	US-09-180-439-8	Sequence 8, Appli
29	150	3.7	1091	3	US-08-986-485-5	Sequence 5, Appli
30	149.5	3.7	342	1	US-08-272-919-2	Sequence 2, Appli
31	149.5	3.7	342	1	US-08-619-916-2	Sequence 2, Appli
32	149.5	3.7	342	5	PCT-US95-08542-2	Sequence 2, Appli
33	149	3.7	605	4	US-09-063-950-5	Sequence 5, Appli
34	145	3.6	330	1	US-08-238-163-2	Sequence 2, Appli
35	145	3.6	523	2	US-08-473-553A-3	Sequence 3, Appli
36	144.5	3.5	673	4	US-09-063-950-2	Sequence 2, Appli
37	144	3.5	220	1	US-07-991-867B-11	Sequence 11, Appl
38	144	3.5	220	1	US-08-107-755A-11	Sequence 11, Appl
39	144	3.5	220	2	US-08-544-332-11	Sequence 11, Appl
40	144	3.5	220	4	US-09-370-861A-11	Sequence 11, Appl
41	141.5	3.5	1196	4	US-08-881-706-2	Sequence 2, Appli
42	140.5	3.4	968	4	US-09-228-986-76	Sequence 76, Appl
43	140.5	3.4	2756	1	US-08-375-709-11	Sequence 11, Appl
44	140.5	3.4	2756	1	US-08-752-929-11	Sequence 11, Appl
45	140.5	3.4	2756	4	US-09-090-793-7	Sequence 7, Appli

## ALIGNMENTS

RESULT 1  
PCT-US95-10509-2

Sequence 2, Application PC/TUS9510509  
GENERAL INFORMATION:

APPLICANT: Campbell, Priscilla  
APPLICANT: Potter, Terry  
APPLICANT: Sawyer, Richard  
APPLICANT: Dreyers, Douglas  
APPLICANT: Freed, John  
TITLE OF INVENTION: INTERNALIN PRODUCTS AND PROCESSES  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, 35th Floor  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.A.  
ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/10509  
FILING DATE: 18 AUGUST 1995  
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Kovarik, Joseph E.  
REGISTRATION NUMBER: 33,005  
REFERENCE/DOCKET NUMBER: 2879-11-PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303/863-9700  
TELEFAX: 303/863-0223

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 746 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-10509-2

Query Match 7.9%; Score 322.5; DB 5; Length 746;  
Best Local Similarity 28.7%; Pred. No. 1.3e-16;  
Matches 109; Conservative 68; Mismatches 172; Indels 31; Gaps 10;

QY 409 DPLQKGLSLPNLETLGICFTPIKIDISPVLOQFKKQLMTKTGVTDYRFLDNMPQLEG 468  
Db 104 DPLKN-----LTNLRLLESSNTISDISALSGLTNLDQDSFGNO-VTDLKPANL/TTLER 157

OY	469	IDISQNNLKDISFLSKYKNLTTLVAADNGIEDIRPLGOLPNIKFVLVSNKISDLSPIAS	528
Dd	158	LDISSNKVSIDISYLAKLTNLESLATINNQISDITPLGITNLDELSLNGNQKDIGTILAS	217
OY	529	LHQLQELHIDNNOITDLSPVSHKESLTVVDLSRNADVLAFLQA-PKLETLMVNDTKVSH	587
Dd	218	LTNLTDDLANNQISNLAPLSGLTKEKTEKLGANQISNISPLAGLTALTNLELNENQED	277
OY	588	LDFLKNPNPILSSLSINRAQLQSLEGIEASSVIVRVEAEGNQIKSLVKDKQGSJTFELDVT	647
Dd	278	ISPISNLKNLTLYLLFYFNINISDISPVSSLTKLQRLEFFYNKKVSDPYSSIANLTNINWLSAG	337
OY	648	GNQLTSLEGVNNEFTALDILSVSKNQLTN-----VNLSKPn--KTVTNIDISHNNIS---	696
Dd	338	HNOISDLPPLANLTRITQLGLNDQAWTNAPVNYKANVSIPTNVKANTGALLIAPATISDCG	397
OY	697	---LADKLNEQHIEPAIAKNFP---AVYESGMVGNGTAEE--KAMATK---AKESAQ	744
Dd	398	SYAEPDITWNLPSTINEVSYTFSQPVTIGKGTTFESGTVTOPLKAIFNAKFHVGDKETTK	457
OY	745	EASESHDYNNHNHTYEDEEGH	764
Dd	458	EV-EAGNLLTEPAKPYKEGH	476

```

RESULT 2
US-08-961-083-182
; Sequence 182, Application US/08961083
; Patent No. 6159469
;
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 182:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-961-083-182

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Db      213  SÖLSYSSTASDNN-----TQSVAKGSTS--KPAKSENQSLKEL--YDSPSAQRYS 261
QY      71  -DDGFILTKDSKILSKTDQGIIVVDHGHSHFIFYADLKG--SPFEYLIP--KGASL--- 121
Db     262  ESDGLVF-DPAKILSRTPNGVAIPHGDHYHFIPYKLSALEEKIARMVPISGTGSTVSTN 320
QY     122  AKP-----AVAQRAASQGTSK-VADPHHHYEFNPADIYAEDALGYTVRHDDHFHYIL 172
Db     321  AKPNEVVSSLGSLSSNPSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIP 380
QY     173  KSSLSGQTQAQAKOVATRLPQTSLSLVSTATANGIPGLHFPSTSDGFQFNGQIGVYTKDSI 232
Db     381  KSNQIGQPTLPNNSLAT--PSPSLPIINGTSH-----EKHEEDGYGFANDRRIAEDESGF 433
QY     233  LVDHHDGHLH 241
Db     434  VMSHGDHNH 442

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RESULT 3
; US-08-961-083-56
; Sequence 56, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 796 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-961-083-56

Query Match          5.5%; Score 223; DB 4; Length 796;
Best Local Similarity 19.5%; Pred. No. 7e-09;
Matches 168; Conservative 116; Mismatches 279; Indels 300; Gaps 42;

QY      30 TYPPIKTKQSRRGMTSNKIKRPIKSSKKTINKTHKGVAAGVDEPTDDGFILTKDSKILSKTDQG 89
       :|: |::| ::| ||::| :||| :| : : |||
DB      1 SYELGLYQARFYKENNRVSYIDGKAQTQRT-ENLTPDEVSKREG--INAEQIVIKITDQG 57
       :|: |::| ::| ||::| :||| :| : : |||

QY      90 IVVDHGHSHFIIFYADLDKGSPEFYLI PKGASLAKPAVAQAASQGTSGKVADPHHHYEFPN 149
       :|: |::| ::| ||::| :||| :| : : |||

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Db      58 YVTSHGHHY-----YNKVPIDAIISELL-----MKDP--NYKLKD   94
QY     150 ADIVAEDALGYTVRHDDHFHYILKSS-----LSGOTQAQAKOVATRLPQTSSLV  198
       ||| | || : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      95 EDIVNEVGKGVIKVDKKYYVLXKAHAHADNVRTKEEINRQKHQSHEREGTPRNDGAV  154
QY     199 STATANGIPGLHEPTSDGFQFNGGGIVGVTKDSILVDHGHLPISFADL-----  248
       : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db     155 ALARSQG----RYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHIYPKNELASASELAAEA  210
QY     249 -----ROG-----GWAHVADQYDPAKAEKPAAETHQTPELSEREKEYO    286
Db     211 FLSGRGNLNSRTRYRRQNDSNDRTNW--VPSVSNGPTNTNTSNTSNSQASGSNDID    268
QY     287 EKLAYL-----AEGIGDPSTIKRVETODGCKLEFPHHDAHVL---MISDIE    332
Db     269 SLLKQLYLPLSQRHVESDGLVEPDPAOI---TSRTARGAVPAPHGDHYHFIPLYSQMSLE    324
QY     333 --IGK DIP---DPHAIEHARELEKHKVMGMTLRALGFDEEVILDIVRTHDAPTPPSNE    386
Db     325 ERARIIPLYRSNHWPDSRP-----EQSPQPTE                               356
QY     387 KDPNMMEKWELATVIKLDGSRKDPLORKGLSLPNL-ETICIGFTPIKDISPVIOFKLK    445
Db     357 PSPGPQP--APNLKIDSNS-----SLVSQLVRAKGEgy-----              387
QY     446 QLMKTQGVTDYRELDMNPOLLEGIDISQNNLKDI-SFLSKYKNL-TLVAADNGTEDIR    502
Db     388 --VFEEKGISRYVEFAKDLR-----SETVKNESKLSQESVSHTLTAKKEN-----VA    433
QY     503 PLGO-----LPNL-----KFVLSNNKISDSLPLASLHQLOELHIDNQITDSPYSHE    552
Db     434 PRDOEFYDKAYNLLTEAHKALEFXNKGRNSDFQALDKL-LERLNDES-----TNKE    482
QY     553 SLTVDLSRNADVDTLATLOAPKLETIMVNDFKVSHLDPLKNNPNLSSLINRAQLOSLEG    612
Db     483 KL--VD-----DLLAF LAP-----ITHPERL-GKPN-----             505
QY     613 IEASSVIYRVEAEGNOIKSLVLKDQGS LTFLDV TGNQ L TS LE G V N N F T A LD I LS VK N Q    672
Db     506 ----SQIEYTEDEVRIAQLADK-----YTTS DGY -IFEHDII SD EG DA          544
QY     673 LTNVNL SKPKVT VN ID SH--NNISLADKL NEQH IPEAI AKN--FPAVYE GSMWG NG    727
Db     545 YVTPHMGH-----SHWICKDSLSD--KEKVAQAQVYTK EKGI LP SP D ADV KAN P    591
QY     728 TAEEKAAMATKAKESAQEASES HDYNHN HT YE DEEGA-----HEHRDK---DHHDH-    776
       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     592 TGDSAALYNRVKGEKR IPLVR L P Y M VE H TE V E V K N G NL I PH KD HY HN IK FA W PD HT YK    651
QY     777 -----EHEDGE 781
Db     652 APNGTYLEDLFATIKYVEHPDE 674

RESULT 4
US-08-961-083-66
; Sequence 66, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigen s and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33

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; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 763 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-961-083-66

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Query Match	5.0%;	Score 204;	DB 4;	Length 763;
Best Local Similarity	19.8%;	Pred. No. 1.9e-07;		
Matches 171;	Conservative 125;	Mismatches 314;	Indels 254;	Gaps 43;

QY	41	GMTSNKIKPIKSSKTKNKT	HKGVAGVDPTDGGFILTKDSKILSKTDGIVVDHGHSHF	100			
		: :   :     :	: : :           :				
Db	29	GÖKAENLTPEVSKREG----	-----INAEÖXVIKITDÖGYVTSHGDIHYH	70			
QY	101	IFYADLKGSPEFYLLIPK	GA\$LA\$KPAVA\$QRAASÖGTSK	VADPHHHYEFNPADIVAEDALGY	160		
		: : :   :   : : :	: : :   : :   :     :				
Db	71	-----YNGKVPYDAI	ISELL-----MKDP--NYÖLKDS	SDIVNEIKGGY	107		
QY	161	TVRHDDHFHYLLKSSLS	GÖTÖAQÖKÖVATRLPÖTS-----	SLVSTATANGIPGLHFP	212		
		: : : :   :   :	: : : : :   :	: : :   :     :			
Db	108	VIKVNGKYYVYLKDA	HAHADNIRTKKEIKRÖKÖERSH	ENSRADNAVAAARAÖG----	RYT	163	
QY	213	TSDFÖFNGÖGIVGVT	KDSILVDHGHLPISFADLRÖG	GAHVADÖYDPAKKA	EKPÄET	272	
		:     :   :   :   :	:   :   :   :   :   : :	:   :   :   :   :   : :			
Db	164	TDDGYIFNASDI	IEDTGDAYIVPHGDHYHI	PKNELSASELA--AAEAYWNG	KÖGSRPSS	222	
QY	273	HÖ-----TPELSER-----	EKEYÖKLA\$YLAEKIGIDPSTIK	RVETÖDÖKL-----		313	
		:	:   : :   :   :   :	: : :   :   :   :			
Db	223	SSYNANPAÖPRLSEN	HNLTVTPTYHÖNÖGENIS	SLREL\$YAKPLSERHVES--	DGLIFDPA	281	
QY	314	-----GLEYPHHDAHVL--	MLSDIE--IGKDI	P-----DPHAIEHARELEK	HKHYGM	356	
		: : :   :   :   : :	: : :   :   :   : :	: : :   :   :   : :			
Db	282	ÖITSRTARGVA	VPHGHHYHFIPYÖMSELEK	RIARITPLKRSNH	WVPDSRPEÖP-----	336	
QY	357	DTLRALGFDEEVL	LDIVRTHDAPRTPPSPNEK	DPNMKEWLATV	IKLIDGSRKDP	LÖRKGL	416
		:       :   :	:       :     :   : :	:       :     :   : :			
Db	337	-----SPÖSTPEP	SPSPÖPAPNPÖP-----	APSNPID	EKL\$VKEAVRKVG	D	376
QY	417	SLLPNLETLGIG--	FTPIKDISPV---LÖFKKLKÖ--	LMTKGV--TD-----		456	
		:   : :   : :   :   :	:   :   :   :   :   :	:   :   :   :   :   :			
Db	377	GYV--FEENGVS	KRYTPAKKDL\$AETAAGID	SKLAKÖESL\$HKLGA	KAKTTDL	PSSDREFYNKA	434
QY	457	YRFLDNMPÖLEGID	I\$ÖNNLKDISFLSKYKN	LTVAADNGIEDIR	PLGÖLPNLK	FIVLS	516
		: :   :   :   : :   :	:   :   :   :   :   :	:   :   :   :   :   :			
Db	435	YDLARIHÖ---DL	DNKGRÖVDF-----	EALDNL	LERIKD-----	VX	469
QY	517	NNKI-----SD	SPLASIHÖLÖELHIDN	NÖITDLSPVSHKES	LTVDLSRNAD	VIDLATIÖA	572
		: :   :   :   :   :   :	: :   :   :   :   :   :	: :   :   :   :   :   :			
Db	470	SDKVKLVXDILAF	LAPIRHPERL	GKPNÄÖITYTD----	DEIÖVAK	LAKGYTTEDGYIFD	524
QY	573	PKLETLMVNDTKV----	SHLDFLKNPNP	NLSSLSINRÄQÖSLE--	GIEASSV----	IVRYE	623
		:   :   :   :   :   :	:   :   :   :   :   :	:   :   :   :   :   :			
Db	525	PRDITSDEGD	AYVTPHMTSHWIKKD--	SL\$EAERAAÖAYAK	EKGGLTPPST	DHÖDSGNT	583





STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/353,585  
FILING DATE: 15-Jul-1999  
CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q 1/68  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/930,277  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: PCT/GB96/00785  
FILING DATE: 01-APR-1996  
APPLICATION NUMBER: GB 9506658.5  
FILING DATE: 31-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Ms Mary J Wilson  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 620-69  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1112 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Tomato  
STRAIN: Cf2  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-353-585-2  
Query Match 4.1%; Score 167; DB 4; Length 1112;  
Best Local Similarity 24.3%; Pred. No. 0.00025;  
Matches 104; Conservative 49; Mismatches 141; Indels 134; Gaps 20;  
QY 396 LATVIKLDGSRKDPLOKRG-----LSLPNLETLGI-----GFTPIKDISPVLQFKKL 444  
DB 118 LTNLVYLDLNNN-----QISGTIPPQIGLAKLQIRIFHNQNGFIP-KEIG-----YL 166  
QY 445 KQLMTKTGVTDYRFLDNMPQLEGIDISQNNLKDIFLSKYKN-----LT 489  
DB 167 RSLTKLSLGI---NLSG-----SIPASVGNLNNLSFLYLYNNQLSGSIPEEISYLSRLT 218  
QY 490 LVAAADNGIEDIRP--LGQLPNLKFVLSNNKIS-----DLS-----524  
DB 219 ELDLSDNALNGSIPASLGNMNNLSFLYLYNNQLSGSIPEEICYLSLTLYDLSENALNGS 278  
QY 525 ---PLASLHQLELHIDNNQITDLS--VSHKESLTVVDLSRNA-----DVDLATLQAPK 574  
DB 279 IPASLGNLNNLSFLYLYNNQLSGSIPEEIGYLSRLNVLGSENALNGSIPASLGNLKNLS 338  
QY 575 LETLMVNDTKVSHLDFLKNPNLSSSL-----SINRAQLQSLLEGIEASSV 618  
DB 339 RLNLVNNQLSGSIIPASLGNLNNLSMLYLYNNQLSGSIIPASLGNLNNLSMLYLYNNQLSGS 398  
QY 619 IYRVEAEGNQLKSLVLKDKQ-----GSLTFLDVYTGNOQLTSL--EGVNNFTALD 664  
DB 399 IPASLGNLNNLSRLYLYNNQLSGSIPEEIGYLSLTLYDLSSNNSINGFIPASFGMSNLA 458  
QY 665 ILSVSKNQLTNVNLSPN-----KVTYNIDISH-----NNISLADKLNE- 704  
DB 459 FLFLYENQLAS---SVPEEIGYLSRLNVLGSENALNGSIPASFGNLLNLSRLNLVNNQL 515

QY 705 -QHIEPAI 711  
DB 516 SGSIPEEI 523  
RESULT 8  
US-09-353-585-3  
Sequence 3, Application US/09353585  
Patent No. 6287865  
GENERAL INFORMATION:  
APPLICANT: Dixon, Mark S  
Jones, David A  
Jones, Jonathan DG  
TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon & Vanderhye PC  
STREET: 8th Floor, 1100 No. 6287865th Glebe Road  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/353,585  
FILING DATE: 15-Jul-1999  
CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q 1/68  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/930,277  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: PCT/GB96/00785  
FILING DATE: 01-APR-1996  
APPLICATION NUMBER: GB 9506658.5  
FILING DATE: 31-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Ms Mary J Wilson  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 620-69  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1112 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Tomato  
STRAIN: Cf2  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-353-585-3  
Query Match 4.1%; Score 167; DB 4; Length 1112;  
Best Local Similarity 24.3%; Pred. No. 0.00025;  
Matches 104; Conservative 49; Mismatches 141; Indels 134; Gaps 20;  
QY 396 LATVIKLDGSRKDPLOKRG-----LSLPNLETLGI-----GFTPIKDISPVLQFKKL 444  
DB 118 LTNLVYLDLNNN-----QISGTIPPQIGLAKLQIRIFHNQNGFIP-KEIG-----YL 166  
QY 445 KQLMTKTGVTDYRFLDNMPQLEGIDISQNNLKDIFLSKYKN-----LT 489  
DB 167 RSLTKLSLGI---NLSG-----SIPASVGNLNNLSFLYLYNNQLSGSIPEEISYLSRLT 218



QY	490	LVAADANGIEDIRP--LGOLPNLKFVLSNNKIS-----DLS-----	524
		: :   :           : :	
Db	219	ELDLSDNALNGSIPASLGNMNNLSFLFYGNQLSGSIPEETCYLRSLTYLDISENALNGS	278
QY	525	---PLASLHQLOELHIDNNQITDLS--VSHKESLTYVDSIRNA----DVDLATLQAPK	574
		: :   :   :   :   :   :	
Db	279	IPASLGNLNNLSFLFYGNQLSGSIPEETCYLRSLNVLGISENALNGSIPASLGNLNL	338
QY	575	LETLMVNDTKVSHLDFLKNPNLSSL-----SINRAQLOSLEGTEASSV	618
		: :             : :   :	
Db	339	RLNLVNNQLSGSIIPASLGNLNNLSMLYLYNNQLSGSIIPASLGNLNNLSMLYLYNNQLSG	398
QY	619	IVRVEAGNQIKSLVLDKQ-----GSLTFLDVYTGNOULTSL--EGVNNFTALD	664
		: :   :   :   :       :   :	
Db	399	IPASLGNLNNLSRLYLYNNQLSGSIPEETCYLSLTYLDLSNNSINGETIPASFGNMENLA	458
QY	665	ILSVSKNQLTNVNLSKPN----KTYVNIIDISH-----NNISLADLKLINE- 704	
		: : :     :   :   : :   :   :	
Db	459	FLFLYENQLAS---SVPEETCYLRSLNVLDSLENALNGSIPASFGNLNNLSRLNLYNNQL	515
QY	705	-QHIEPAT 711	
		:	
Db	516	SGSIPEET 523	

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RESULT 9
US-09-228-986-72
; Sequence 72, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 72
; LENGTH: 910
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-228-986-72

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Query Match	4.0%;	Score 165;	DB 4;	Length 910;
Best Local Similarity	23.9%;	Pred. No. 0.00026;		
Matches	90;	Conservative 63;	Mismatches 114;	Indels 110;
				Gaps 17;
QY 416	LSLLPNLETLGIGFTPIKDISP-----VLOFKKLKOLMTKGTVDYRFLDMPQLEG	468		
	: :   :     :   : : :   :			
Db 171	LCLLPNLICMSLGINNLTGTTPDCLGNISSLOYLSQGNQGSVPSE--LGRLSQLIIV	227		
QY 469	IDISQNNLKDI--SFLSKYKNTLVAAADNGIEDIRPLQLEN-----LKFVLVLSN	517		
	:  :  :  :  :  :  :  :  :  :  :  :  :  :			
Db 228	LDLFGNHLTGCIPISSLNCTNELLDIDGNQL-----VGHIPSHLCTKTTQOLMYRLGA	282		
QY 518	NKISDLSL--LASLHQLQELHIDNNQITDLSL-----VSHKESLTVVDSLNRADVDLATL	570		
	:  :  :  :  :  :  :  :  :  :  :  :  :			
Db 283	NQLSGSVPSLFNCTKIQEIALPYNQLSGIVPMELGKLTHLQRLF--EGGNVYFISGNTM	339		
QY 571	QAPKLETLMVNDTKVSHLDFLKN-----PN	596		
	:  :  :  :  :  :  :  :  :  :  :  :  :			
Db 340	RCPIIL-TALSNCSLDLYVDLSENNFTGQLPFSIGHLSKLIYHLDSNELAGEIIPPAIGN	398		
QY 597	LSSLUI-----NRAQLQSLEGI--EASSVIVRVEAEGNQIKSLVCLKDKGS	640		
	:  :  :  :  :  :  :  :  :  :  :  :			
Db 399	LSLTLFLNLGRNYFTGSISSLIMLOKLERLYMDSNNLQGNIPMETIGQLKSLGL-----	452		
QY 641	LTFEDVTGNQLTSL--EGVNNFTALDILSVSKNQLT--NVNLSKPNKTVTNIDISHNNI	695		
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Db 453	--LYLSGNNLSGKIPDEFVANTLOQLRYLYLNHNQLSGDINANLGKCVNLLI--LDLSYNKL	508		

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QY      696 SLADLKNEQHIPEAIA 712
          |      +11: :|
Db      509 S-----CHIPQELA 517
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RESULT 10
; US-09-180-439-3
; Sequence 3, Application US/09180439
; Patent No. 6225532
; GENERAL INFORMATION:
; APPLICANT: Dixon, Mark S
; APPLICANT: Hatzixanthis, Kostas
; APPLICANT: Jones, David A
; APPLICANT: Jones, Jonathan DG
; TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof
; FILE REFERENCE: 620 - 53
; CURRENT APPLICATION NUMBER: US/09/180,439
; CURRENT FILING DATE: 1998-12-06
; EARLIER APPLICATION NUMBER: PCT/GB97/01249
; EARLIER FILING DATE: 1997-05-08
; EARLIER APPLICATION NUMBER: GB 9609681.3
; EARLIER FILING DATE: 1996-05-09
; EARLIER APPLICATION NUMBER: GB 9619924.5
; EARLIER FILING DATE: 1996-09-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 968
; TYPE: PRT
; ORGANISM: Lycopersicon esculentum
US-09-180-439-3

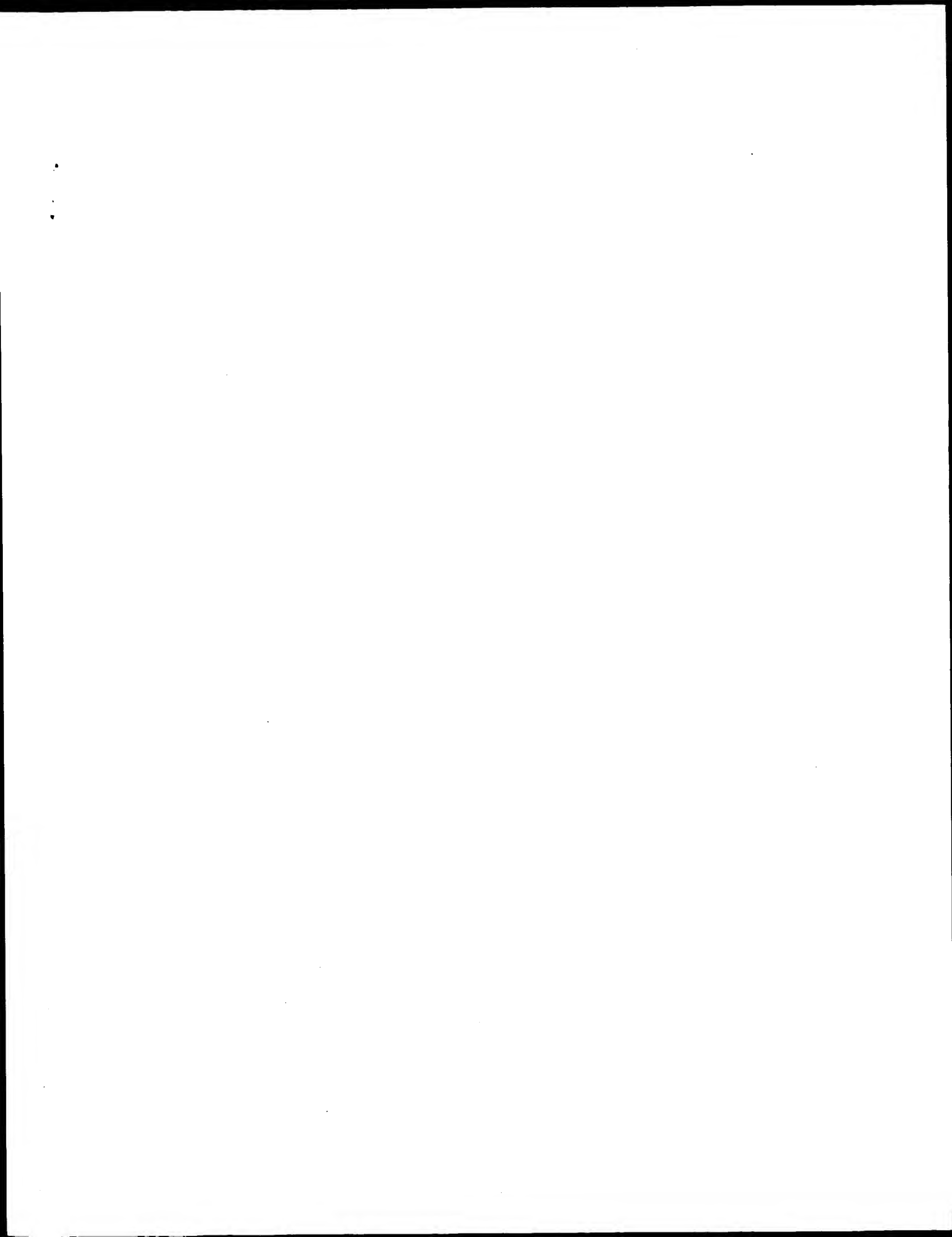
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[illegible]











GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 19, 2003, 07:51:03 ; Search time 227.541 Seconds

(without alignments)  
335.715 Million cell updates/sec.

Title: US-09-645-835A-4

Perfect score: 4080

Sequence: 1 MKTKKVIILVGLLSSQLTL.....DHDHEDENEAKDEQNHAD 792

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

Total number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	292.5	7.2	1039	9	US-09-884-465A-6 Sequence 6, Appli
2	292.5	7.2	1152	9	US-09-884-465A-379 Sequence 379, App
3	292.5	7.2	1238	9	US-09-884-465A-381 Sequence 381, App
4	292.5	7.2	1365	9	US-09-884-465A-382 Sequence 382, App
5	292.5	7.2	1378	9	US-09-884-465A-378 Sequence 378, App
6	241	5.9	715	9	US-09-252-088-16 Sequence 16, Appl
7	241	5.9	793	9	US-09-252-088-15 Sequence 15, Appl
8	233	5.7	447	10	US-09-765-272-182 Sequence 182, App
9	224.5	5.5	840	9	US-09-884-465A-10 Sequence 10, Appl
10	224	5.5	838	9	US-09-884-465A-8 Sequence 8, Appl
11	223	5.5	796	10	US-09-765-272-56 Sequence 56, Appl
12	204	5.0	763	10	US-09-765-272-66 Sequence 66, Appl
13	201.5	4.9	2026	10	US-09-801-368-86 Sequence 86, Appl
14	195	4.8	1119	9	US-09-905-291A-294 Sequence 294, App
15	195	4.8	1119	9	US-09-902-853-294 Sequence 294, App
16	195	4.8	1119	9	US-09-907-824-294 Sequence 294, App
17	195	4.8	1119	9	US-09-907-841-294 Sequence 294, App
18	195	4.8	1119	9	US-09-904-011-294 Sequence 294, App
19	195	4.8	1119	9	US-10-028-072-352 Sequence 352, App

20	195	4.8	1119	9	US-09-906-742-294 Sequence 294, App
21	195	4.8	1119	9	US-10-121-049-352 Sequence 352, App
22	195	4.8	1119	9	US-10-123-904-352 Sequence 352, App
23	195	4.8	1119	9	US-10-140-470-352 Sequence 352, App
24	195	4.8	1119	9	US-09-906-838-294 Sequence 294, App
25	195	4.8	1119	9	US-09-907-613-294 Sequence 294, App
26	195	4.8	1119	9	US-09-907-942-294 Sequence 294, App
27	195	4.8	1119	9	US-10-175-746-352 Sequence 352, App
28	195	4.8	1119	9	US-10-176-918-352 Sequence 352, App
29	195	4.8	1119	9	US-10-176-921-352 Sequence 352, App
30	195	4.8	1119	9	US-10-137-865-352 Sequence 352, App
31	195	4.8	1119	9	US-10-140-474-352 Sequence 352, App
32	195	4.8	1119	9	US-09-904-820-294 Sequence 294, App
33	195	4.8	1119	9	US-09-904-859-294 Sequence 294, App
34	195	4.8	1119	9	US-09-909-204-294 Sequence 294, App
35	195	4.8	1119	9	US-10-142-431-352 Sequence 352, App
36	195	4.8	1119	9	US-10-143-114-352 Sequence 352, App
37	195	4.8	1119	9	US-09-904-786-294 Sequence 294, App
38	195	4.8	1119	9	US-09-906-646-294 Sequence 294, App
39	195	4.8	1119	9	US-09-906-700-294 Sequence 294, App
40	195	4.8	1119	9	US-10-140-002-352 Sequence 352, App
41	195	4.8	1119	9	US-09-902-903-294 Sequence 294, App
42	195	4.8	1119	9	US-09-903-749A-294 Sequence 294, App
43	195	4.8	1119	9	US-09-903-786-294 Sequence 294, App
44	195	4.8	1119	9	US-10-142-419-352 Sequence 352, App
45	195	4.8	1119	9	US-09-902-736-294 Sequence 294, App

ALIGNMENTS

RESULT 1  
US-09-884-465A-6  
; Sequence 6, Application US/09884465A  
; Publication No. US20030077293A1  
; GENERAL INFORMATION:  
; APPLICANT: Shire Biochem, Inc.  
; APPLICANT: Hamel, Josee  
; APPLICANT: Brodeur, Bernard  
; APPLICANT: Martin, Denis  
; APPLICANT: Charland, Nathalie  
; APPLICANT: Ouellet, Catherine  
; TITLE OF INVENTION: Streptococcus Antigens  
; FILE REFERENCE: 055190-0044  
; CURRENT APPLICATION NUMBER: US/09/884,465A  
; PRIOR FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: 60/212,683  
; PRIOR FILING DATE: 2000-06-20  
; NUMBER OF SEQ ID NOS: 384  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 1039  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
; US-09-884-465A-6

Query Match 7.2%; Score 292.5; DB 9; Length 1039;  
Best Local Similarity 21.4%; Pred. No. 2.1e-10;  
Matches 185; Conservative 114; Mismatches 283; Indels 283; Gaps 45;

QY 16 SQTLLIACSGRNGTYPPIKTKQSRKMTSNKIKPIKSKTKTKHKGAVGVDFPT----- 70  
DB 237 SQTLSYSTASDNN-----TQSVAKGSTS---KPANKSENLSLKLKEL--YDSPSAQRYS 285  
QY 71 -DDGFILTRKSKILSKTDQGIIVVDHGDHSHFIFYADLKG--SPEFYLLP---KGASL--- 121  
DB 286 ESDGLVF-DPAKISRTPNGVAILPHGDHYHIFPYSKLSALEEKIARMVPISGTSTVSTN 344  
QY 122 AKP-----AVAQRAASQGTSK-VADPHHMYEFNPADIYAEDALGYTVRHDDHFIYL 172  
DB 345 AKPNEVYSSLGSLSSNPSSLTFSKELSSASDGYIFNPKDIYEETATATAYIVRHGHFIYIP 404  
QY 173 KSSLGQTQAQAKQVATRLPQTSLSLVSTATANGIPGLHPTSDGFQFNGGCIYGVTKDSI 232

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Db 405 KSNQIGOPTLPNNSLAT--PSPSLPINPGTSH-----EKHEEDGYGFDANRILIAEDES GF 457
QY 233 LVDDHGHLPISFADLRQGGWAHVADQYDPAKKAEPETHOT----- 275
Db 458 VMSHGDHNNHYFEKKDLTE-----EQIKAQKHLEEVKTSNGLDLSLSEHDYPC 507
QY 276 --PELSEREKEYOEKLAELAELGIDPSTIKRVETQDGKLGLEYPHHDAHVLMLSDIEI 333
Db 508 NAKEMKDLKKIEEKIAGIMKQYGVKRESTI---VVNKEKNAILIYPHGDH----- 553
QY 334 GKDIPDPHAIHARELEKHK--VGMDTLRALGFDEEYILDIVRTHDAPTPPSSNE---KD 388
Db 554 -----HHADPIDEHKPVG-----IGHSHSNYELFKPEEGVAKKE 587
QY 389 PNMM--KEWLATVIKLDIGSRKDPLOKGLSLPNELETGIGFTPIKDISPVLQFKKLKQ 446
Db 588 GNKYVTGEELTNVNL---LKNSTFNNQNTLANGOKRVSPSPPELE-----KKG I 637
QY 447 LMTKTGVTDYRFLD-----NMPQLEG---IDISQNNLKDISFLS 483
Db 638 NMLVKLITPDGKVLKESGKVEGEGVGNIANFELDQYLLPGQTFKYTTASKDYPEVS YDG 697
QY 484 KYKNLTIVA-----AANGIEDIRPLGOLP-NLKFLV-----LSNN 518
Db 698 TETVPTSLAYKMASQTIFFYPFHAGDTYLR--VNPQFAVPKGTDALVRVDEFHGNAYLENN 756
QY 519 -KISDLS-PLASLHQ-----LOELHIDNNO--ITDLSPVSHKESLTVVDLS 560
Db 757 YKVGELIKLPIPKLNQGTTRFAGCNKIPVTFMANAYLDNOSTYIVEV-PILEKENQT----- 810
QY 561 RNADVDLATLQAPKLETLMVNDTKVSHLDLFLKNNPN-LSSLINRAQLOSL--EGIEASS 617
Db 811 -----DKPSILPQFKRNKAQENSKLDEKVEEPPK 838
QY 618 VIVRVEAE-----GNQIKSLVLKD-----KQSLTFLDVYG---NQLTSLEGVNNFT 661
Db 839 TSEKVEKEKLESETGNSTNSSTLEEVPTVDVQEKVAKFAESYGMKLENVLFNMDG----- 893
QY 662 ALDILSVSKNQLTNVNLSPKPKTVTNIDISHNNISLADLKLNEQHIPEAIAKNFPAYVEG 721
Db 894 -----TIELYLPSEGV---IKKN---MADF---TGEAPQNGENKPS--EN 928
QY 722 SMVNGTAEKAAAMATKAKESAQEA 746
Db 929 GKVSTGTVENQPT-ENKPADSLPEA 952

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RESULT 2  
US-09-884-465A-379  
Sequence 379, Application US/09884465A  
Publication No. US2003007293A1

GENERAL INFORMATION:  
APPLICANT: Shire Biochem, Inc.  
APPLICANT: Hamel, Josee  
APPLICANT: Brodeur, Bernard  
APPLICANT: Martin, Denis  
APPLICANT: Charland, Nathalie  
APPLICANT: Ouellet, Catherine  
TITLE OF INVENTION: Streptococcus Antigens  
FILE REFERENCE: 055190-0044  
CURRENT APPLICATION NUMBER: US/09/884,465A  
PRIOR FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: 60/212,683  
NUMBER OF SEQ ID NOS: 384  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 379  
LENGTH: 1152  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Unknown Organism

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; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa = Methionine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (344)..(344)
; OTHER INFORMATION: Xaa = Glycine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (345)..(345)
; OTHER INFORMATION: Xaa = Proline or nothing
; US-09-884-465A-379

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Query Match 7.2%; Score 292.5; DB 9; Length 1152;  
Best Local Similarity 21.4%; Pred. No. 2.4e-10;  
Matches 185; Conservative 114; Mismatches 283; Indels 283; Gaps 45;

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QY 16 SOLTLACQSRGNGTYPITKQSRKGMTSNKIKPIKSKTKNTKHKGVAGVDEPT----- 70
Db 350 SOLSYSSIASDNN-----TQSVAKGSTS--KPAKSENLSQSLKEL--YDSPAQRYS 398
QY 71 -DDGFILTKDSKILSKTDQGIYVDDHGHSHFIYADLKG--SPFEYLIP--KGASL--- 121
Db 399 ESDGLVF-DPAKIISRTPNGVAIPHGDHYHFIYPSKLSALEEKIARMVPISGTGSTVSTN 457
QY 122 AKP-----AVAQRAASQGTSK-VADPHHHYEFNPADIVAEDALGYTVRHDDHPHYIL 172
Db 458 AKPNEVVSSLSGLSSNPSLTSKELSSASDGYIFNPKDYEETATAYIVRHGDHHPHYIP 517
QY 173 KSSLSCGTQAOAKQVATRLPQTSLSVSTATANGIPGLHFPSTSDGFQNGQIGVYTKDSI 232
Db 518 KSNQIGOPTLPNNSLAT--PSPSLPINPGTSH-----EKHEEDGYGFDANRILIAEDES GF 570
QY 233 LVDDHGHLPISFADLRQGGWAHVADQYDPAKKAEPETHOT----- 275
Db 571 VMSHGDHNNHYFEKKDLTE-----EQIKAQKHLEEVKTSNGLDLSLSEHDYPC 620
QY 276 --PELSEREKEYOEKLAELAELGIDPSTIKRVETQDGKLGLEYPHHDAHVLMLSDIEI 333
Db 621 NAKEMKDLKKIEEKIAGIMKQYGVKRESTI---VVNKEKNAILIYPHGDH----- 666
QY 334 GKDIPDPHAIHARELEKHK--VGMDTLRALGFDEEYILDIVRTHDAPTPPSSNE---KD 388
Db 667 -----HHADPIDEHKPVG-----IGHSHSNYELFKPEEGVAKKE 700
QY 389 PNMM--KEWLATVIKLDIGSRKDPLOKGLSLPNELETGIGFTPIKDISPVLQFKKLKQ 446
Db 701 GNKYVTGEELTNVNL---LKNSTFNNQNTLANGOKRVSPSPPELE-----KKG I 750
QY 447 LMTKTGVTDYRFLD-----NMPQLEG---IDISQNNLKDISFLS 483
Db 751 NMLVKLITPDGKVLKESGKVEGEGVGNIANFELDQYLLPGQTFKYTTASKDYPEVS YDG 810
QY 484 KYKNLTIVA-----AANGIEDIRPLGOLP-NLKFLV-----LSNN 518
Db 811 TETVPTSLAYKMASQTIFFYPFHAGDTYLR--VNPQFAVPKGTDALVRVDEFHGNAYLENN 869
QY 519 -KISDLS-PLASLHQ-----LOELHIDNNO--ITDLSPVSHKESLTVVDLS 560
Db 870 YKVGELIKLPIPKLNQGTTRFAGCNKIPVTFMANAYLDNOSTYIVEV-PILEKENQT----- 923
QY 561 RNADVDLATLQAPKLETLMVNDTKVSHLDLFLKNNPN-LSSLINRAQLOSL--EGIEASS 617
Db 924 -----DKPSILPQFKRNKAQENSKLDEKVEEPPK 951
QY 618 VIVRVEAE-----GNQIKSLVLKD-----KQSLTFLDVYG---NQLTSLEGVNNFT 661
Db 952 TSEKVEKEKLESETGNSTNSSTLEEVPTVDVQEKVAKFAESYGMKLENVLFNMDG----- 1006
QY 662 ALDILSVSKNQLTNVNLSPKPKTVTNIDISHNNISLADLKLNEQHIPEAIAKNFPAYVEG 721
Db 1007 -----TIELYLPSEGV---IKKN---MADF---TGEAPQNGENKPS--EN 1041
QY 722 SMVNGTAEKAAAMATKAKESAQEA 746

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Db 563 SQLSYSTASDNN-----TQSVAKGSTS---KPAKSENLOSLKEL--YDSPAQRYS 611
QY 71 -DDGFILTKDSKILSKTDGIVVDHDSHFIFYADLK--SPFEYLIP---KGASL--- 121
Db 612 ESDGLVF-DPAKISRTPNGVAIPHGDHVFIPYKLSALEEKIARMVPISGTGVSTN 670
QY 122 AKP-----AVAQRAASQGTSK-VADPHHHYEFNPADIVAEDALGYTVRHHDFHYIL 172
Db 671 AKPNEVVSSLSGLSSNPSSLTTSKELSSASDGYTFNPKDIVEETATAYIVRGDHFHYIP 730
QY 173 KSSLGQTOAQAKQVATRLPQTSLSVSTATANGIPGLHPTSDGFQFNGQIGVTKDSI 232
Db 731 KSNQIGQPTLPNNSLAT--PSPSLPINPGTSH----EKHEEDGYGFDANRIIAEDESCE 783
QY 233 LVDHGHLPISFADLRQGGWAHVADQYDPAKKAEPETHQT----- 275
Db 784 VMSHGDNHNYFFKKDLTE-----EQIKAAQKHLEEVKTSNGLDLSLSEHDYDPG 833
QY 276 --PELSEREKEYOEKLAFLAELGIDPSTIKRVETODGKLGLEYPHHDAHVMLSDIEI 333
Db 834 NAKEMKDLDKKIEKTAGIMQYGVKRESI---VVNKEKNAIIPYHGDH----- 879
QY 334 GKIDPPHAIHARELEKHK-VGMDTLRALGFDEEVLIDIVRTHDAPTPPSPNE---KD 388
Db 880 -----HHADPIDEHKPVG-----IGHSHSNYELFKPEEGVAKKE 913
QY 389 PNMM--KEWLATVIKLDGSRKDPLOKGLSLPNLETLGIGFTPIKDISPVLQFKLKQ 446
Db 914 GNKYVTGEELTNVNL--LKNSTFNNQNTFLANGQKRVSEFSFPELE-----KGLGI 963
QY 447 LLMTKTGVTDYRFLD-----NMPQLEG---IDISQNNLKDISFLS 483
Db 964 NMLVKLITPDGKVLKESGVGEVGNIANFELDQPYLPQGTFTKTYTIAASKDYPEVSYDG 1023
QY 484 KYKNLTLVA-----AANGIEDIRPLGOLP-NLKFLV-----LSNN 518
Db 1024 TFTVPTSLAYKMASQTIFFYPFHAGDTYLR-VNPQFAVPKGTDALVRVDFEFGNAYLENN 1082
QY 519 -KISDLS-PLASLHQ-----LOELHIDNNQ--ITDLSPVSHKESLTVVDLS 560
Db 1083 YKVGEEKLPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYIVEV-PILEKENQT----- 1136
QY 561 RNADVDLATLQAPKLETLMVNDTKVSHDLFLKNPN-LSLSLNRALQOLSL--EGIEASS 617
Db 1137 -----DKPSILPQFKRNKAQENSKLDEKVEEPK 1164
QY 618 VIVRVEAE-----GNQIKSLVLKD-----KOGSLTFLDVYG---NQLTSLEGVNNFT 661
Db 1165 TSEKVEKEKLESTGNSTSNSTLEEVPTVDVQEKVAKFAESYGMKLENVLFNMDG----- 1219
QY 662 ALDILSVKNQLTNVNLSKPNKTYTNIDISHNNISLADKLNEQHIPEAIKAFPAVEEG 721
Db 1220 -----TIELYPSGEV-----IKKN---MADE---TGEAPQNGENKPS--EN 1254
QY 722 SMVNGTAEKAKAMATKAKESAQEA 746
Db 1255 GKVSTGTVENOPT-ENKPADSLPEA 1278
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RESULT 5

US-09-884-465A-378

; Sequence 378, Application US/09884465A

; Publication No. US20030077293A1

; GENERAL INFORMATION:

; APPLICANT: Shire Biochem, Inc.

; APPLICANT: Hamel, Josee

; APPLICANT: Brodeur, Bernard

; APPLICANT: Martin, Denis

; APPLICANT: Charland, Nathalie

; APPLICANT: Ouellet, Catherine

; TITLE OF INVENTION: Streptococcus Antigens

; FILE REFERENCE: 055190-0044

; CURRENT APPLICATION NUMBER: US/09/884,465A

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; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 378
; LENGTH: 1378
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa = Methionine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (570)..(570)
; OTHER INFORMATION: Xaa = Glycine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (571)..(571)
; OTHER INFORMATION: Xaa = Proline or nothing
; US-09-884-465A-378
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## Query Match

Best Local Similarity 21.4%; Score 292.5; DB 9; Length 1378;

Matches 185; Conservative 114; Mismatches 283; Indels 283; Gaps 45;

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QY 16 SOLTLIACQSRGNGTYPIKTKQSRKGMTSNKIKPIKSSKTKNTHKGAVGVDFPT----- 70
Db 576 SQLSYSTASDNN-----TQSVAKGSTS---KPAKSENLOSLKEL--YDSPAQRYS 624
QY 71 -DDGFILTKDSKILSKTDGIVVDHDSHFIFYADLK--SPFEYLIP---KGASL--- 121
Db 625 ESDGLVF-DPAKISRTPNGVAIPHGDHVFIPYKLSALEEKIARMVPISGTGVSTN 683
QY 122 AKP-----AVAQRAASQGTSK-VADPHHHYEFNPADIVAEDALGYTVRHHDFHYIL 172
Db 684 AKPNEVVSSLSGLSSNPSSLTTSKELSSASDGYTFNPKDIVEETATAYIVRGDHFHYIP 743
QY 173 KSSLGQTOAQAKQVATRLPQTSLSVSTATANGIPGLHPTSDGFQFNGQIGVTKDSI 232
Db 744 KSNQIGQPTLPNNSLAT--PSPSLPINPGTSH----EKHEEDGYGFDANRIIAEDESCE 796
QY 233 LVDHGHLPISFADLRQGGWAHVADQYDPAKKAEPETHQT----- 275
Db 797 VMSHGDNHNYFFKKDLTE-----EQIKAAQKHLEEVKTSNGLDLSLSEHDYDPG 846
QY 276 --PELSEREKEYOEKLAFLAELGIDPSTIKRVETODGKLGLEYPHHDAHVMLSDIEI 333
Db 847 NAKEMKDLDKKIEKTAGIMQYGVKRESI---VVNKEKNAIIPYHGDH----- 892
QY 334 GKIDPPHAIHARELEKHK-VGMDTLRALGFDEEVLIDIVRTHDAPTPPSPNE---KD 388
Db 893 -----HHADPIDEHKPVG-----IGHSHSNYELFKPEEGVAKKE 926
QY 389 PNMM--KEWLATVIKLDGSRKDPLOKGLSLPNLETLGIGFTPIKDISPVLQFKLKQ 446
Db 927 GNKYVTGEELTNVNL--LKNSTFNNQNTFLANGQKRVSEFSFPELE-----KGLGI 976
QY 484 KYKNLTLVA-----AANGIEDIRPLGOLP-NLKFLV-----LSNN 518
Db 1037 TFTVPTSLAYKMASQTIFFYPFHAGDTYLR-VNPQFAVPKGTDALVRVDFEFGNAYLENN 1095
QY 519 -KISDLS-PLASLHQ-----LOELHIDNNQ--ITDLSPVSHKESLTVVDLS 560
Db 1096 YKVGEEKLPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYIVEV-PILEKENQT----- 1149
QY 561 RNADVDLATLQAPKLETLMVNDTKVSHDLFLKNPN-LSLSLNRALQOLSL--EGIEASS 617
Db 1150 -----DKPSILPQFKRNKAQENSKLDEKVEEPK 1177
```











```

: NUMBER OF SEQUENCES: 452
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Human Genome Sciences, Inc.
: STREET: 9410 Key West Avenue
: CITY: Rockville
: STATE: Maryland
: COUNTRY: USA
: ZIP: 20850
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
: COMPUTER: HP Vectra 486/33
: OPERATING SYSTEM: MSDOS version 6.2
: SOFTWARE: ASCII Text
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/765,272
: FILING DATE: 22-Jan-2001
: CLASSIFICATION: <Unknown>
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/961,083
: FILING DATE: <Unknown>
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Brookes, A. Anders
: REGISTRATION NUMBER: 36,373
: REFERENCE/DOCKET NUMBER: PB340P2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (301) 309-8504
: TELEFAX: (301) 309-8512
:
: INFORMATION FOR SEQ ID NO: 56:
:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 796 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-765-272-56

Query Match      5.5%; Score 223; DB 10; Length 796;
Best Local Similarity 19.5%; Pred. No. 3.8e-06;
Matches 168; Conservative 116; Mismatches 279; Indels 300; Gaps

QY      30 TYPRIKTQSRKGMTSNKTIPIKSKKTKNTKHKGVAGVDFPDDGFIILTKDSKILSKTDQG 89
      :|: |:| :|:|: |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db      1 SYELGLYQARTVKENNRVSIIDGQATQKT-ENLTPDEVSKREG--INAEQIVIKITDQG 57

QY      90 IVDHDGSHFIFYADLKGSPFEYLIPKGLASLAKPAVAQRAASQGTSKVADPHHHYEFNP 149
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      58 YVTSHGDIHY-----YNGKVPYDAIISELL-----MKDP--NYKLKD 94

QY      150 ADIVAEDALGYTVRHDDHRYILKSS-----LSGQTQAQAQAVATRLPQTSSLV 198
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      95 EDIVNEVGKGYVIKVDGKYVYLLKDAHADNVRTKKEIINRQKQEHSHQREGGTPRNDGAV 154

QY      199 STATANGIPGLHFTSDGFQFNGGIVGVTKDSILVDHGHLPISFADL----- 248
      : | : | : | | | | | | | | | | | | | | | | | | | | | | | |
Db      155 ALARSQG---RYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNELASASELAALAA 210

QY      249 -----RQG-----GMAHVADQYDPAKKAKEPAETHQTPELSEREKEYQ 286
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      211 FLSGRGLNSRTRYRQNSDNTSRTNW--VPSVSNPGTTNTNTSNNSTNSQASQSDNDID 268

QY      287 EKLAYL-----AEKLGIDPSTIKRVETQDGKLGLEYPHHDAHVL--MLSDIE 332
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      269 SLLKQLYKLPISQRHVESDGLVEDPAQI---TSRTARGVAVPHGDHYHFIPYSQMSLE 324

QY      333 --IGKDIP---DPHAIEHARELEKHKVGMDTLRALGFDEEVLIDIVRTHDAPTFPSNE 386
      | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      325 ERIARIIPLRYSRNMHWVDSRP-----EQSPSPQPTPE 356

QY      387 KDPNMMKEWLATVIKLDLGSRKDPLQRKGLSLPNL-ETLGIGTPIKDISPVLQFKKLK 445
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      357 PSPGPQP--APNLKIDSNS-----SLVSQLVKRVKGEY----- 387

```

[illegible]

Query Match	5.0%;	Score 204;	DB 10;	Length 763;
Best Local Similarity	19.8%;	Pred. No. 5.7e-05;		
Matches 171;	Conservative 125;	Mismatches 314;	Indels 254;	Gaps 43;

QY	41	GMTSNKIKPIKKSCKTNKTHKGVAGVDEFTDDGFIITLKDSKILSKTDQGIIVVDHDSHF	100
Db	29	GQKAENLTPEVSKREG-----INAEQXVLIKTTDQGYVTSHGDXHY	70
QY	101	IFYADLKGSPEFYLI PKGASLAKPAVAQRAASQGSTKVADPHNHYEFPADIYAEDALGY	160
Db	71	-----YNGKVPYDAIISELL-----MKDP--NYQLKSDSDIVNELKGCY	107
QY	161	TVRHDDHFHYILKSSLSGQTQAQAKQVATRLPQTS-----SLVSTATANGIPGLHFP	212
Db	108	VIKVNGKYVYVYLKDAHADNIRTKKEELIKROQERSHNHNSRADNAVVAARAQC---RYT	163
QY	213	TSDGFOFNGQGIYGVTKDSILVDHDSHLHPISFADLRQGGNAHVADQYDPAKKAEPAT	272
Db	164	TDDGYIFNASDIEDTGDAYIVPHGDHYHYIPKNELSAEELAAEAYWNGKQSGRPPSS	222
QY	273	HQ-----TPELSEK-----EKEYQEKLAYLAEKLGDIPSTIKRVETODGKL---	313
Db	223	SSYNANPAQPELSENNHNLVTPTYHONOGENISSLLRELYAKPLSERHVES-DGLIFDPA	281
QY	314	-----GLEYPHDDAHVL--MLSDIE--IGKDIP----DPAIEHARELEKHVGM	356
Db	282	QITSRTARGAVAPHGNHYHFIPYEQMSELEKRIARILPRKRSNHWPDSRPEQ-----	336
QY	357	DTLRALGFDEEVLIDIVRTHDAPTPPSPNEKDPNMMEMLATVTKLDLGSRKDPQLQRKL	416
Db	337	-----SPQSTPEESPSPQAPNPQP-----APSNPIDEKLYKAVRKVGD	376
QY	417	SLLPNLETLGIG-FTPIKDISPV-----LQFKKLKQ-LMTKTGV--TD-----	456
Db	377	GYV--FEENGVSRYIPAKDLSAETIAGIDSKLAKQESLSHKLGAKKTTDLPPSSDREFYNTKA	434
QY	457	YRFLDNMPOLEGIDISQNNLKDISFLSKYKNLTLVAADNGIEDIRPLGQLPNLKEVLVS	516
Db	435	YDLLARIHQ-----DLDDNKGROYDF-----EALDNLLERLKD-----VX	469
QY	517	NNKI-----SDLSPLASLHOLQETHIDNNQITDLSPVSHKESLTJVVDSRNADVDLATLQA	572
Db	470	SDKVKLYXDILAFIAPIRHPERLQKPNQAQITYTD-----DEIQVAKLAGKTYTDEGYIFD	524
QY	573	PKLETLMAVNDTKV---SHDLFLKNPNPLSSLSINRAQLQSLE-GIEASSV---IVRVE	623
Db	525	PRDITSDGDAYVTPHMTSHMWIKKD-SLSEAERAAQAAYAKEGLTPRPIDHODSGNTE	583
QY	624	AEG-----NOIKS-----LVLKDKQSGSL-----TFLDVTGNQL	651
Db	584	AKGAEAITYNRVKAAKKVPIDRMPYNLQYTYVEYKNGSLIIRHYDHYHNKFEWFD-----	637
QY	652	TSLEGV---NNFTALDILSVSKNQLTNVNLSPKNKTVTNIDISHNNISLADKLNEQHI	707
Db	638	---EGDYEARPKGYTLLEDLATVKKYVEHPN-ERPHS-----DNGFGNAS-----DHV	680
QY	708	PEALAKNFPAYVEGSMVGNCT---AEKKAAMATRAKESAQEAASESHD--YNNHNTYEDEE	762
Db	681	QR--KNK-----GQADTNQTEKPSSEKQTEKPEEETPREKKQSEKRPESPKEETPEE	732
QY	763	GHAHEHRDKDDHDEHEDENEAKD	786
Db	733	SPEESEEPQVETEKVEEKLREAAD	756

RESULT 13  
US-09-801-368-86

```

; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 86
; LENGTH: 2026
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-86

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Query Match	4.9%;	Score 201.5;	DB 10;	Length 2026;
Best Local Similarity	19.0%;	Pred. No. 0.00032;		
Matches 156;	Conservative 138;	Mismatches 289;	Indels 239;	Gaps 33;

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QY 34 KTRQSRKGMTSNKIKPIK---KSKTKNTKHKVAGVDEPTDGGFILLTKDSKILSKTDQGI 90
Db 480 RSKSRRSSIDADELDPMSPPSPSKKDSRHNDH-----RKDNESM 518
QY 91 VVDHDGSHFIEFYADLKGSPEYLLIPKGASTAKPAVAQARAOSGTSKVADPHNHYEFPNA 150
Db 519 VTAGDSNSSFV---DI---CKENVPND---SKTALDTKSVNRLKSNLAMSPPSIRYAPS 568
QY 151 DIVAEDALGYIVRHDDHFHYILKSSLGQ-----TQAAQAVATR-----LPQ 193
Db 569 NLDDGYDTSSTSS-----LPSSSISEDTSSCSDSSSYTNAYMEANREQDNKTPILNK 622
QY 194 TSSLVSTATANGIPGLHPTSDGFQFNGOGIVGVTKDSILVDHDGHLHPISFADLRGGW 253
Db 623 TKSYTKKFTSSV---NMNSPDGAQSSGLLQDEKDEVEQLEHYHKDFSDDLPRKHYA 679
QY 254 AHVADQYDPAKKAE-KPAETHQTPELSEKEKEYQEKLAYLAEKLGDIPSTIKRVETQDGK 312
Db 680 IRIFNTDFTFTLCTPATY-----VEEIIPALKRKFENITAQGNFQISLKVKG 727
QY 313 LG-----LE-----YRHHDAHVLMLSDIE-IGKDIPDPHAIEH-----A 346
Db 728 LSKILRPTSKPILIERKLLLLNGYRKSDPRLHMGIEDLSFVFKFLFHPVTPSHFTPEQ 787
QY 347 RELEKHVKYMDTLRALGFDEEVLIDIVRTHDAFTPRPSNEKDPNMKEMLATVIKL----- 402
Db 788 RIMRSEFVHYD-LRNMDLTPPIEFQHTSEIESLSDVSNMNAIFLPLEFISSIKLLSLR 846
QY 403 --DLGSRKDP-----LQKGLSLPN-----LETLGIGFT 430
Db 847 MVNIRASKFSPSINITKAYKLVSELOQNFIRKVPNSIMKLSNLTILNLQCNELSESLPAGF- 905
QY 431 PIKDISPVLOFKKLIKQLMTKTGYTDY---RFLDNMPQEGIDISQNNLKDISPLSKY- 485
Db 906 -----VELKNLQLLDLSSNKEMHYPEVINYCTNLLQ---IDLSYNKIQSLPQSTKYL 954
QY 486 KNLTLVAADNGIEDIRPLGQLPNKFLVLSNNKISDLSPLASLHQLQELHIDNNOITDL 545
Db 955 VKLAKMNLSHKNLNFIGDLSEMTDLRTILNRYNRISSIKTNAS--NLQNLFTDNRIISNF 1012
QY 546 SPVSHKESLTVVDLSRNADVDLATLQAPKLETLMVNDTKYSHLDFLKNP-NLSSISNR 604
Db 1013 EDT-----LPKLRALIEIQENPTISISFKDFYPKNMTSLTNK 1049

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QY      605 AQLSLGIEASSVIVREAEGNQIKSLVLKDKQSLFLDVTGNQLTSL-EGVNNFTAL 663
      ||| | : |      | | | : | : | | | : | : | |
Db      1050 AQLSSIPG-----ELTTKLSFLEKLELNQNNLTRLPQEISKLTKL 1089

QY      664 DILSVSKNQLTNV--NLSKPNKTVTNIDISHNNI-----SLADKLNEQHIPEAIARNFP 716
      ||| : | : | : | : | : | : | : | : | : | : |
Db      1090 VFLSVARNKLEYIRPELSQ-LKSLRTLDDLHSNNIRDFVDGMENLELTSLNI----- 1139

QY      717 AVEGSMVGNGTAEKAMATKAKESAQEAASESHDYNHNHTY 758
      : | | : |      : | | : |
Db      1140 ---SSNAFGNSSLE-----NSFYHNMST 1159

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RESULT 14
US-09-905-291A-294
: Sequence 294, Application US/09905291A
: Patent No. US20020160374A1
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, A..
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth, J.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.
: TITLE OF INVENTION: secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/905,291A
: CURRENT FILING DATE: 2001-07-12
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: 2000-02-22
: PRIOR APPLICATION NUMBER: US 60/143,048
: PRIOR FILING DATE: 1999-07-07
: PRIOR APPLICATION NUMBER: US 60/145,698
: PRIOR FILING DATE: 1999-07-26
: PRIOR APPLICATION NUMBER: US 60/146,222
: PRIOR FILING DATE: 1999-07-28
: PRIOR APPLICATION NUMBER: PCT/US99/20594
: PRIOR FILING DATE: 1999-09-08
: PRIOR APPLICATION NUMBER: PCT/US99/20944
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/21547
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/23089
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: PCT/US99/28214
: PRIOR FILING DATE: 1999-11-29
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: 1999-11-30
: PRIOR APPLICATION NUMBER: PCT/US99/28564
: PRIOR FILING DATE: 1999-12-02

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; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 294
;
; LENGTH: 1119
;
; TYPE: PRT
;
; ORGANISM: Homo Sapien
US-09-905-291A-294

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Query Match          4.8%; Score 195; DB 9; Length 1119;
Best Local Similarity 21.6%; Pred. No. 0.00036;
Matches 105; Conservative 90; Mismatches 149; Indels 142; Gaps 23;

QY   286 QEKIAYLAEKIGIDPSTIKRVETQDGKLGLEYPHHDAHVLMSDIEIGKDIPDPHAIEH 345
      ::||| | | | | : : : : | : : : : | : : : : | : : : : | : : : :
Db    62 RKRRLARLEPL---PSWVARLDLS-----HNRLSFIKASSMS-----HLQS 99

QY   346 ARELEKHKKVGMDTLRALGFDEEVILDIVRTHDAPTPFPSSNEKDPNNMKEWLATVIKLDG 405
      ||:: : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db    100 LREKVLNNELETIPNLG-----PVSAN-----ITLSSL-AG 130

QY   406 SRKDPLQRKGLSLPNLETLGICFTPIKDISPVLQFKKLQMLMKTGVTDYR--FLDN- 462
      : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db    131 NRIVELLPEHLKEFQSLETTDLSSNNISELOTAFPALQLKYLYLNSNRVTSMEPGYFDNL 190

QY   463 -----MPLEGIDISQNCLKDISFLS----KYKNLTLVAAA 494
      : ||| : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db    191 ANTLVLVKLNRRNRISAIPPCKMFKLPOQLHLELNRRNKIKNVGDGLTFQGLGALKSLKM--Q 247

QY   495 DNGIEDIR--PLGQLPNLKFLVLSNNKISDLS--LASLHQLELHDNNQITDLSPVSH 550
      || : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db    248 RNGVTKMDGAFWGLSNMEILLQLDHNNLTEITKGWLGYGLMLQELHLSONAINRISPDAW 307

QY   551 K--ESTIVVDLSRN---ADVDLATLQAPKLETLMVNDTKVSH-----LDF 590
      : : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db    308 EFCQKLESELDLTFNHLRLD-DSSFGLSLNTLPHIGNNRVSXIADCAFRGLSSIKTLD- 365

QY   591 LKNNPNLSLSINRAQLOSLEGIFASSIVRVEAEGNQIKSLVLKDKQG--SLTFLDVTG 648
      , ||| : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db    366 LKNNELSWITEDMNGAFSGLDKLR-----RLIQGNRIRSITKKAFTGLDALHLLDLS 419

QY   649 NQLTSLEGVNNFTALDILSVSKNQLTNVNLSKPNTVTNIDISHNNISLADKLENEQHHP 708
      | : | : | : | : : : : | : : : : | : : : : | : : : : | : : : :
Db    420 NAIMSLQG-NAFS-----QMKKLQQLHLNTSS-----LLDCQL--KWLP 456

QY   709 EAIAKN 714
      : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db    457 QWVAEN 462

RESULT 15
US-09-902-853-294
; Sequence 294, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
```



```

: APPLICANT: Gerltsen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth, J.
: APPLICANT: Kijavin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/902,853
: PRIOR APPLICATION NUMBER: US/09/665,350
: PRIOR FILING DATE: 2000-09-18
: PRIOR APPLICATION NUMBER: US 60/143,048
: PRIOR FILING DATE: 1999-07-07
: PRIOR APPLICATION NUMBER: US 60/145,698
: PRIOR FILING DATE: 1999-07-26
: PRIOR APPLICATION NUMBER: US 60/146,222
: PRIOR FILING DATE: 1999-07-28
: PRIOR APPLICATION NUMBER: PCT/US99/20594
: PRIOR FILING DATE: 1999-09-08
: PRIOR APPLICATION NUMBER: PCT/US99/20944
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/21547
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/23089
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: PCT/US99/28214
: PRIOR FILING DATE: 1999-11-29
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: 1999-11-30
: PRIOR APPLICATION NUMBER: PCT/US99/28564
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/28565
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: PCT/US99/30911
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US99/30999
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US00/00219
: NUMBER OF SEQ ID NOS: 423
: SEQ ID NO 294
: LENGTH: 1119
: TYPE: PRT
: ORGANISM: Homo Sapien
: US-09-902-853-294

```

Query Match 4.8%; Score 195; DB 9; Length 1119;  
 Best Local Similarity 21.6%; Pred. No. 0.00036;  
 Matches 105; Conservative 90; Mismatches 149; Indels 142; Gaps 23;

```

QY 286 QEKLAYLAELGIDPSTIKRVETQDGKLGUEYRPHDHAHVLMSTIFIGKDIIPDPAIEH 345
Db 62 RKRLARLPEPL---PSWVARLDLS-----HNRLSFIKASSMS-----HLQS 99

QY 346 ARELEKHKVGMDTLRALGFDEEVLIDIVRTHDAPTFPSNEKDPNMKKEWLATVIKLDLG 405
Db 100 LREVKLNNELEETIPNLG-----PVSAN-----ITLSTL-AG 130

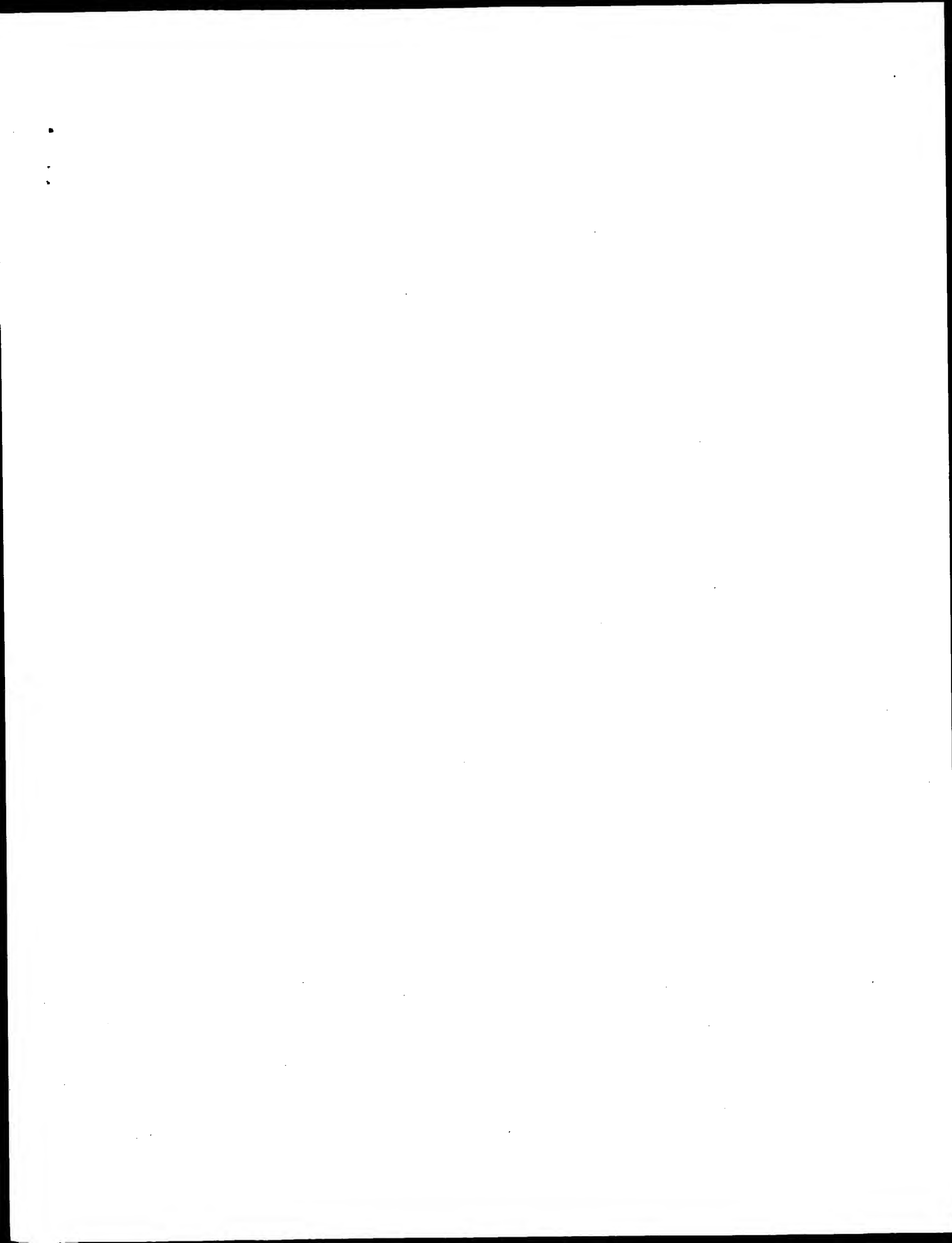
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QY 406 SRKDPLOQRKGLSLPNELETIGFTPIKDISPYVQFKKLQMLMTKTGYTDYR--FLDN- 462
Db 131 NRIVEILPEHLKEFQSLFTLIDSSNNISELQTAEPALQKLKYLINSNRVTSMEPGYFDNL 190
QY 463 -----MPLEGIDISQNNLKDIFLS-----KYNLTVA 494
Db 191 ANTLVLKLNRRNISAIPEPKMFKLQDLHLELNKIKVNDGLTFQIGALKSLKM---Q 247
QY 495 DNGIEDIR--PLGOLPMLKFLVLSNNKISDLS--LASLHLOELHIDNNQITDLSVSH 550
Db 248 RGVTKLMDGAFWGLSNMEILQDLHNNLTFTTKGWLGLMLQELHLSQNAINRISPDW 307
QY 551 K--ESLTVVDSRN---ADVDLATLQAPKLETIMVNDTKVSH-----LDF 590
Db 308 EFCQKLSLDTTFNHLRLD-DSSFLGLSLNTLHIGNNRVSIADCAFRGLSLKTLT- 365
QY 591 LKNPNLSSLSINRAQLQSLGIEASSVIVRVEAGNQIKSLVLKQOG--SLTFLDVTG 648
Db 366 LKNEISWTIEDMNGAFSGLDKLR-----RLIQGNRIRISTTKAFTGLDALEHLDSD 419
QY 649 NQLTSLEGVNNFTALDILSVSKNQLTNVNLSPKNTVTNIDISHNNTSLADKLNEQHIP 708
Db 420 NAIMSLQG-NAFS-----QMKKLQQLHNTSS-----LLDCQL--KWL 456
QY 709 EAIK 714
Db 457 QWVAEN 462

```

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 Job time : 239.541 secs



GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2003, 07:51:03 ; Search time 12.7448 Seconds

(without alignments)  
1883.841 Million cell updates/sec

Title: US-09-645-835A-7

Perfect score: 4265

Sequence: 1 MKINKKYLVSAAALILSVC.....KLALLKGSNPSSVSKEKIN 816

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/5A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4163	97.6	796	US-08-961-083-56	Sequence 56, Appl
2	2661.5	62.4	763	US-08-961-083-66	Sequence 66, Appl
3	1186.5	27.8	447	US-08-961-083-182	Sequence 182, App
4	162	3.8	3696	US-09-134-001C-5080	Sequence 5080, Ap
5	160	3.8	10182	US-09-134-001C-3159	Sequence 3159, Ap
6	152	3.6	783	5231168-2	Patent No. 5231168
7	147	3.4	812	US-09-513-783A-6	Sequence 6, Appli
8	145.5	3.4	1073	US-09-541-782-6	Sequence 6, Appli
9	145.5	3.4	1073	US-09-723-820-6	Sequence 6, Appli
10	144	3.4	1040	US-08-961-083-118	Sequence 118, App
11	142.5	3.3	2314	US-09-816-703A-2	Sequence 14, Appl
12	140	3.3	1503	US-08-976-255-14	Sequence 2, Appli
13	140	3.3	2431	US-07-920-281C-2	Sequence 2, Appli
14	140	3.3	2431	US-08-466-277-2	Sequence 22, Appl
15	137.5	3.2	1610	US-09-513-783A-22	Sequence 4, Appli
16	136	3.2	812	US-09-513-783A-4	Sequence 32, Appl
17	136	3.2	1056	US-09-513-783A-32	Sequence 5, Appli
18	135.5	3.2	740	US-08-257-073-5	Sequence 2, Appli
19	135.5	3.2	1183	US-08-447-031A-2	Sequence 1, Appli
20	135	3.2	2308	US-08-015-973-1	Sequence 1, Appli
21	135	3.2	2308	US-08-448-164-1	Sequence 1, Appli
22	135	3.2	2308	US-08-081-929-2	Sequence 2, Appli
23	133.5	3.1	1507	5268270-2	Patent No. 5268270
24	133.5	3.1	1664	US-09-599-652-2	Sequence 2, Appli
25	133.5	3.1	1664	US-08-642-846-2	Sequence 2, Appli
26	133.5	3.1	1664	US-09-264-604-2	Sequence 2, Appli
27	133	3.1	1093	PCT-US93-03077-1	Sequence 1, Appli

28	132	3.1	1164	4	US-09-457-708-2	Sequence 2, Appli
29	132	3.1	1338	1	US-08-471-033-50	Sequence 50, Appl
30	132	3.1	1338	2	US-08-471-044-50	Sequence 50, Appl
31	132	3.1	1338	2	US-08-463-483A-50	Sequence 50, Appl
32	132	3.1	1338	2	US-08-471-046A-50	Sequence 50, Appl
33	132	3.1	1338	2	US-08-470-566B-50	Sequence 50, Appl
34	132	3.1	1338	2	US-08-469-334-50	Sequence 50, Appl
35	132	3.1	1338	3	US-09-300-529-50	Sequence 50, Appl
36	131.5	3.1	2032	4	US-09-071-035-458	Sequence 458, App
37	131.5	3.1	2032	4	US-09-071-035-462	Sequence 462, App
38	131.5	3.1	2032	4	US-09-071-035-466	Sequence 466, App
39	130.5	3.1	1435	2	US-08-568-459A-4	Sequence 4, Appli
40	130.5	3.1	1435	2	US-08-487-826B-4	Sequence 4, Appli
41	130.5	3.1	1435	4	US-09-210-288-4	Sequence 4, Appli
42	130	3.0	2115	4	US-09-324-867-5	Sequence 4, Appli
43	129	3.0	688	3	US-09-141-047-8	Sequence 8, Appli
44	129	3.0	2860	2	US-08-826-267-2	Sequence 2, Appli
45	128.5	3.0	916	1	US-08-188-228-48	Sequence 48, Appl

## ALIGNMENTS

RESULT 1  
US-08-961-083-56  
; Sequence 56, Application US/08961083  
; Patent No. 6159469  
; GENERAL INFORMATION:  
; APPLICANT: Choi et. al.  
; TITLE OF INVENTION: Streptococcus pneumoniae Antigenes and Vaccines  
; NUMBER OF SEQUENCES: 452  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961,083  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB340P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 796 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-961-083-56  
Query Match 97.6%; Score 4163; DB 4; Length 796;  
Best Local Similarity 99.9%; Pred. No. 2.2e-305;  
Matches 795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 21 SYELGLYQARTVKENRVSIDGKQATQKTENLTPDEVSKREGINAEOIVIKITDQGYVT 80  
Db 1 SYELGLYQARTVKENRVSIDGKQATQKTENLTPDEVSKREGINAEOIVIKITDQGYVT 60

```

QY 81 SHGDHYHYNGKVPYDAIISEELMKDPNYKLKDEDIVNEVGKGYIKVDGKYVYVLKDA 140
Db 61 SHGDHYHYNGKVPYDAIISEELMKDPNYKLKDEDIVNEVGKGYIKVDGKYVYVLKDA 120
QY 141 AHADNVRTKEEINRQKQEHSHQREHREGTTPRNDGAVALARSGRYTTDDGYIFNASDIIEDT 200
Db 121 AHADNVRTKEEINRQKQEHSHQREHREGTTPRNDGAVALARSGRYTTDDGYIFNASDIIEDT 180
QY 201 GDAYIVPHGDHYHYIPKNELSASELAEEAFLSGRNLNSRTYRRONSDNTSRTNWPS 260
Db 181 GDAYIVPHGDHYHYIPKNELSASELAEEAFLSGRNLNSRTYRRONSDNTSRTNWPS 240
QY 261 VSNPGTTNTNTSNNSTNSQASQSDNDISLKLQLYKLPLSQRHVESDGLVDPQAQITSTRT 320
Db 241 VSNPGTTNTNTSNNSTNSQASQSDNDISLKLQLYKLPLSQRHVESDGLVDPQAQITSTRT 300
QY 321 ARGVAVPHGDHYHYIPYSQMSLEERIRIIPLRYSNHWVPDSRPEQSPQPTPEPSPG 380
Db 301 ARGVAVPHGDHYHYIPYSQMSLEERIRIIPLRYSNHWVPDSRPEQSPQPTPEPSPG 360
QY 381 PQPAPNLKIDSNSLSVQSLVRKVGEGYVEEEKISRYVFAKDLPSSETVKNLESKLSKQES 440
Db 361 PQPAPNLKIDSNSLSVQSLVRKVGEGYVEEEKISRYVFAKDLPSSETVKNLESKLSKQES 420
QY 441 VSHTLTAKKENAVAPRDQEFYDKAYNLLTEAHKALFENKGRNSDFQALDKLLERLNDESTN 500
Db 421 VSHTLTAKKENAVAPRDQEFYDKAYNLLTEAHKALFENKGRNSDFQALDKLLERLNDESTN 480
QY 501 KEKLVDDLAFAPITRPERLGKPNQIEYTEDEVRIAQALADKYTTSDGYIFDEHDIISD 560
Db 481 KEKLVDDLAFAPITRPERLGKPNQIEYTEDEVRIAQALADKYTTSDGYIFDEHDIISD 540
QY 561 EGDAYVTPHMGSHWIGKDSLSDEKVAQAAYTKKEGILPPSPDADYKANPTGDSAAAIY 620
Db 541 EGDAYVTPHMGSHWIGKDSLSDEKVAQAAYTKKEGILPPSPDADYKANPTGDSAAAIY 600
QY 621 NRVKGEKRIPLVRLPYMEHTVEVKNGLIIPKHDYHNKIFAWFDDHTYKAPNGYTTLED 680
Db 601 NRVKGEKRIPLVRLPYMEHTVEVKNGLIIPKHDYHNKIFAWFDDHTYKAPNGYTTLED 660
QY 681 LEATIKYVEHPDERPHSDGNGNASEHVLGKKHSDSDPNKNFKADEEPEVETPAEPEVP 740
Db 661 LEATIKYVEHPDERPHSDGNGNASEHVLGKKHSDSDPNKNFKADEEPEVETPAEPEVP 720
QY 741 QVETEKVEAQLKEAEVLLAKVTDSSLKANATEETLACLRNNLTQIMDNNSITMAEAELKLA 800
Db 721 QVETEKVEAQLKEAEVLLAKVTDSSLKANATEETLACLRNNLTQIMDNNSITMAEAELKLA 780
QY 801 LKGSNPPSSVSKEKIN 816
Db 781 LKGSNPPSSVSKEKIN 796

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; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 763 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-961-083-66

Query Match 62.4%; Score 2661.5; DB 4; Length 763;
Best Local Similarity 66.8%; Pred. No. 3.1e-192;
Matches 520; Conservative 78; Mismatches 131; Indels 49; Gaps 8;

QY 20 CSYELGLYQARTV-KENNRVSYIDGQATQKTENLTPEVSKREGINAEOIVIKITDQGY 78
Db 1 CSYELGRHQAGQVKRESNRYSIDGQAGQKAENLTPEVSKREGINAEOIVIKITDQGY 60
QY 79 VTSHGDIHYHYNGKVPYDAIISEELMKDPNYKLKDEDIVNEVGKGYIKVDGKYVYVLK 138
Db 61 VTSHGDIHYHYNGKVPYDAIISEELMKDPNYQLKSDDIVNEIKGGYIKVNGKYVYVLK 120
QY 139 DAHADNVRTKEEINRQKQEHSHQREHREGTTPRNDGAVALARSGRYTTDDGYIFNASDIIE 198
Db 121 DAHADNVRTKEEIKRQKQEHSHQREHSHNS--RADNAVAARAQGRYTTDDGYIFNASDIIE 177
QY 199 DTGDAYIVPHGDHYHYIPKNELSASELAEEAFLSGRNLNSRTYRRONSDNTSRTNWV 258
Db 178 DTGDAYIVPHGDHYHYIPKNELSASELAEEAYWNG-----KQGSRRSSSSSYN 226
QY 259 PVSNSPGTTNTNTSNNSTNSQASQSDNDISLKLQLYKLPLSQRHVESDGLVDPQAQITS 318
Db 227 ANPAQPRUSENNHNTLVTPTYHQ--NOGENISSLLRELVAKPLSERHVESDGLVDPQAQITS 285
QY 319 RTARGVAVPHGDHYHYIPYSQMSLEERIRIIPLRYSNHWVPDSRPEQSPQPTPEPS 378
Db 286 RTARGVAVPHGNHYHYIPYEQMSLEERIRIIPLRYSNHWVPDSRPEQSPQPTPEPS 345
QY 379 PGQPAPAPNLK-IDSN---SSLSVQSLVRKVGEGYVEEEKISRYVFAKDLPSSETVKNLESK 434
Db 346 PSPQPAPAPNPQAPSNPIDKLVKEAVRKVGDDGYVEENGVSRYIPAKDLSETAAGIDSK 405
QY 435 LSKQESVSHTLTAKKENAVAPRDQEFYDKAYNLLTEAHKALFENKGRNSDFQALDKLLERL 494
Db 406 LAKQESLSHKLGAKTDLPSSDREFYNAKAYDLARIHQDLDNKGRQVDFEALDNLLERL 465
QY 495 NDESTNKEKLVDDLAFAPITRPERLGKPNQIEYTEDEVRIAQALADKYTTSDGYIFDE 554
Db 466 KDVSXSDKVLVXDILAFAPIRHPERLGKPNQIYTTTDEIQVAKLAGKYTTEDGYIFDP 525
QY 555 HDIISDEGDAYVTPHMGSHWIGKDSLSDEKVAQAAYTKKEGILPPSPDADYKANPTGD 614
Db 526 RDITSDEGDAYVTPHMTSHWIKKDSLEAERAAQAAYAKKEKGLTPSTDHQDSGNTAEAK 585
QY 615 SAAAIYNRVKGEKRIPLVRLPYMEHTVEVKNGLIIPKHDYHNKIFAWFDDHTYKAPN 674
Db 586 GAEAIYNRVKAAKKVPLDRMPYNLQTYVEVKNGLIIPHYDHYHNKIFEWFDGELYEARP 645
QY 675 GYTLEDLLEATIKYVEHPDERPHSDGNGNASEHVLGKKHSDSDPNKNFKADEE----- 728

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RESULT 2
US-08-961-083-66
; Sequence 66, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2

```

```

Db      646  GYTLDELLATVKKYVEHPNERPHSDNGFGNASDHWQRRKNKGADTNQTEKPESEKPTQTEK 705
      729  PVEET-----PAPEVPQVETEKYEAOIKEAEVLLAKVTD 763
QY      706  PEEETPREEKROSEKESPSPKPTPEEESPSESEEPQVETEKYEKELREAEDLLGIQIOD 763
Db

```

### RESULT 3

```

US-08-961-083-182
; Sequence 182, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigenes and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
;
; FILING DATE:
;
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
;
; FILING DATE:
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
;
; INFORMATION FOR SEQ ID NO: 182:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
US-08-961-083-182

```

	Query Match	27.8%;	Score 1186.5;	DB 4;	Length 447;	
	Best Local Similarity	41.0%;	Pred. No. 2.1e-81;			
	Matches 263;	Conservative 62;	Mismatches 110;	Indels 207;	Gaps 11;	
QY	24	LGLYQARTVKENNRSVSYIDGKQATQKTENTLTPDEVSKREGINAQIVIKITDQGVTSHG	83			
Db	1	LNQHSQENKDNRRSVSYVDGSQSQSENLTTPDVQSQKEIGIAEQIIVIKITDQGYVTSHG	60			
QY	84	DHYHYNGKVPIDAIISEELMKDPNYKLKDEDIVNEVGKGVIKYDGKYYVYLKDAAHA	143			
Db	61	DHYHYNGKVPIDALFSEELMKDPNYQLKDADIVNEVGKGIYIKVDGKYYVYLKDAAHA	120			
QY	144	DNVRTKEEINRQKQEHSHQHRREGTPRNDGAVALARSQGRYTDDGYIFNASDIIEDTGDA	203			
Db	121	DNVRTKEEINRQKQEHVKNDE----KVNSNVAVARSQGRYTINDGYVFNPADIIEDTGNA	176			
QY	204	YIVPHGDHYHIYPKNELSASELAALAEAFLSGRGNLSRTYRKRONSDNTSRTNWVPVSVN	263			
Db	177	YIVPHGGHYHIPKSDSLASELAAKAHLAGKNMQPSQLSYSSTASDN-----	224			
QY	264	PCTTNNTSNSNTNSQASQSDIDSLLKQLYKLPLSQRHVESDGLVFDPAQTSTRARG	323			

[illegible]

## RESULT 4

```

US-09-134-001C5080
; Sequence 5080, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5080
; LENGTH: 3696
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5080

```

	Query Match	3.8%;	Score 162;	DB 4;	Length 3696;
	Best Local Similarity	18.5%;	Pred. No. 0.0098;		
	Matches 183;	Conservative 141;	Mismatches 348;	Indels 316;	Gaps 42;
QY	35 NNRVSYI-DGKQATQKTENTLPDEVSKEGINAEQIVIKITD-----QGVTSHGDHYH	87			
Dd	1299 NNQIDGIVSDGRQSINA---ITPPTSTKRNAKN--DIDIKAADKKIKIQRINDATDEEIQ	1353			
QY	88.YNNGKVPEYDAIISEELMKDPNKLDDEDIVNEVKGVVIKD-----	130			
Dd	1354 EANKRIE-----EAKIEAKDNIGQRNSTRDQVNEAKTINGINKIENTIPATTVKSEARQAVQ	1408			
QY	131 ---GKYVVYLKDAHADNVRTKETENR-----QKQEHSSQHREGC--TPRNDGAVALA	177			
Dd	1409 NKANEOINHIOQTTPDATNEEKQEALNPVSASELARVOAQINAEHTTQCQKTIKDDAITSL	1468			
QY	178 RSQGRYTDDGYIFNASDIIEDTGDAIVPHGDHYHIPKNELSASLAAEAFLSGRG	237			
Dd	1469 R-----INAQVEKE-----SARMA	1483			
QY	238 LSNSTRYRKQ---NSDNTS-----RTNWVPVSXNPGTNTN- -TSNNSNTNSQASQSD	286			
Dd	1484 IEOKATOQTQTFINNNDNATDEEEKVANNLVIATKOXSOLDNISLSNNDEVENAKVAGINE	1543			



QY	287	IDSLLKQLYKPLPSQRHVESDGLVDPDA-QITSRTARGVAVPHGDHYHETIPYSQMSLEEE	345
Db	1544	IANVL-----PATAVSKAKKDIDQKLAQOINQIQTHQATTEE	1582
QY	346	RIARIPLRYSNH-----WVPSRPEQSPQPNP---	375
Db	1583	KEAAIQLANQKSNEARFATIQNEHSNNGVAQAKSNGIHETELVMPDAHKKSDAKQSIDNKY	1642
QY	376	-EPSPGQPAPNLKIDSNSSLVSQL--VRKVGEGYVEEEKISRIVFAKDLPSETYKNLE	432
Db	1643	NEQSNITINTTPDATDEKOKALDKLIKADGAGYKNKVDQAQTNQOVSDAKTEADITITNIQ	1702
QY	433	SKLSKQESVSHTLTAKKE-----NVAPRDQE-----FYDKAYNLL-----	467
Db	1703	ANVAKKPSARVELDSKFEDLKRQINATPNATEEEKQDAIQRLNGKRDEVKNLINQDRDN	1762
QY	468	-TEAHK-----ALFEKNGRNSDFQALDKLLERL-----NDESTNKEKLVDDL	509
Db	1763	EVEQHKNIGLQOLETIANPNTRKSD--ALQELQTKFISQTELINNNKDATNEEK--DEA	1817
QY	510	AFLAPITHPERL-----GKPNQIEYTEDE--VRIAQL-----ADKYTTSQGYIFDEH	555
Db	1818	KRLLEISKNKTTITNINOQTNNQVNDNAKNGMNEIATIIIPATTIKTDAKTAIDKRAEQV	1877
QY	556	DIISDEGDAYVTPHMGSHWIGKDSLDSKEKVAQAQYTKKEGILPSPDADAVKANPTGDS	615
Db	1878	TIINGNDA-----TDEEKAEARKLVEKAKI-----EAKSNTINS	1913
QY	616	AAAIYNRVKGEKRIPLYRLPYVEHTVEVKNGNLIIPKHGDHYHNKIFAWFDDHTYKAP--	673
Db	1914	TE---REVNGAKTNGLEKINNIOPTQTKTNAKQELINDKAQEOQLIQINNTPDATTEEEKOE	1970
QY	674	-----NGYTLDEL-----PATIKYVEHPDERP--HSNDGWNAS	706
Db	1971	ATNRVNAGLAQAIQININNAHSTQEVNESKTSIATIKSVQPNVIKKPTAINSLTQOANNQ	2030
QY	707	EHVLGKKDHSEDPNKNF-----KADE--EPVEETPAEPEVPQVETEKVEA-----Q	750
Db	2031	KTLIGNDGNATDDEKEAAKQLVTQKLNQOIKIHESQDNQVNDVKAQDAITAIKLINANA	2090
QY	751	LKEAEVL-----LAKYTDSSLKAN--AT-----ETLAGLRNNL-----TLQIMD	787
Db	2091	HKRODAINILTNLAESKSDIRANQDATTTEEKNTAIQSIDDTLAQAARNNINGANTNALVD	2150
QY	788	NNSIMAEAEKLLALKGSPSSVSKEKI	815
Db	2151	EN-LEDGOKQLQRIYVLSQTQTKQAKADI	2177

```

RESULT 5
US-09-134-001C-3159
; Sequence 3159, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3159
; LENGTH: 10182
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3159

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Query Match	3.8%;	Score 160;	DB 4;	Length 10182;
Best Local Similarity	18.8%;	Pred. No. 0.068;		

Matches 189; Conservative 126; Mismatches 368; Indels 320; Gaps 43;

QY	33	KENNRSYIDGKQATQKTENTLTPDEVSKREGIN-----AEQIVIKITDQGYVTS	82
Db	5419	ÖKSGEESLVNGSNTSRSEVE-----EHLNEAKSLNNAMKQLRDKVAEKTNVK-QSSDYINDS	5473
QY	83	GDHYHYNGKV-PYDAIISE-----ELMK-----DPNYKLKDEDIVNEVKGGYI	127
Db	5474	TEHÖRGYDOALQEAENIINEIGNPTLNKSEIEOKLQOLTDAQNALQSGHLLFEAKNNAIT	5533
QY	128	KVDGKYVYVLKDAH--ADNVRTKEEINRQKQEHSGHREGCTPRND----GAVALARS	179
Db	5534	GIN--KLTAINDAQÖKAKAIENVOAQÖTIPAVNOQLTLDBREINTAMQALRDKVGQÖQNNVHQ	5591
QY	180	ÖGRYTTDDGYIFNASDIIEDTGDAVIVPHGDHYHYIPKNEL--SASELAAAEAFISGRGN	237
Db	5592	ÖSNYFNEDEQPKHNYDNSVOAQÖTIIIDKLQD--PIMKNKEIEQALINQINTQTALSGENK	5649
QY	238	L-----SNSRTYRRQNSDNTSRTNWVPSVSNPGTNTNTNSNSNTNSQASQSDNDIDSLK	292
Db	5650	LHTDQESTNRQIEGLSSLNTAQAINAEKDLVNOAKTRIDVA-----ÖKLAAKEINSAMS	5703
QY	293	QLYKPLSQRHVESDGLVIEDPAQITSRTARGVAVPHGDHYHIFIPYSÖMSELEERTARIIP	352
Db	5704	NL-----RDGI-----ÖNKEDIKRSSAYINADPTKVATAYDQALQMAENIINATP	5747
QY	353	LKRSNHWVPDSRPEQSPPOPTPEPSPGPÖPAPNLKIDSNSSLVSQLYRKVGEGYVEEK	412
Db	5748	-----NYELNKATIEQALSrvQÖAQÖ-DLD	5771
QY	413	GISRVEFAKDLPSETVKNLES-----KLKQESVSHPTLAK	448
Db	5772	GVQÖLANAKQÖATQTVNGCNSINDGÖKRELNLINSANTRTKVQÖELINKATELNHAMEAL	5831
QY	449	KENVAPRD-----QEFYDKAYNLTTEAHKALFENKGRNSDFQÄLDKLER	493
Db	5832	RNSVQNVDOVKQSSNYVNEQDPEQHNYDNVN--EAQATINNNAQÖVLDKLAIERLTQ	5888
QY	494	LN--DESTNKEKLVDDLAFAPITHPERLGKPNQÖIEY-----TEDEV-R-IAQ---	539
Db	5889	VNTTKDALHGAÖKLTQDQÖAAETGIRGLTSLNEPÖKNAEYAKVTAATTREDEVNRITQÖEAT	5948
QY	540	-----LADKYTT--SDGYIFDEHD-----IISDEGDAYVPHMGH	572
Db	5949	TLDTAMLGRLKRSIKDKNDTKNSSKYINEDHDQÖQAYDNVANNNAQÖVIDETQATLS----	6003
QY	573	SHWIGKDSLDEKEVAQAÖVTKKEGILPPSPDADYKANPTGDSA--AAIYNRYKGEKR	628
Db	6004	-----SDTINQLANAVTQAKSNL--HGDTKLÖHDKDSAKÖTIAQÖLQNLNSAQKH	6050
QY	629	-----IPLVRLPYMVEH-----TVEVKNGNLI--IPKHDIYH-	658
Db	6051	MEDSLIDNESTRQVQHDLTEAQALDGLMGALKESIKDYTNIVSNGYINAEPSSKQAYD	6110
QY	659	-----NIKAFWDDHTY-KAPN--GYTLEDL---	681
Db	6111	AAVQNAQNIINGTNOPTINKGNVTTATQTVKNTKDALDGDHRLEAKNNANQITIRNLNL	6170
QY	682	-----FATIKYVEHPDERPHSNDGWSNASEHYLGKKDH-----SEDP	719
Db	6171	NNAQÖDAEKNLVNSASTLEQVQÖNLQTAQÖLDNAMGELRÖSI-AKKDQVKADSKYLINEP	6229
QY	720	NKNFKADE-----EPVEETPAEPEVPQÖVETEKVEAQÖLKEAEVLL--AKVTDSLSKANATE	772
Db	6230	ÖIKÖNYDDAVQÖRVETITNETÖNPPELLKANIDQATQÖSVQNAEQALHGAEKLNDQÖTSSTE	6289
QY	773	TLAGLRNLTLOIMDNNSIMAEAEKLLALLKGSNPPSSVSKKI	815
Db	6290	-LDGL-TDLT-----DQÖREKLREQÖINTSNSRDDIKÖKI	6321

RESULT 6  
5231168-2



QY	777 LRNNLTQ-----IMDNNSIMAEAEKLALLKGSNPPSSVSKEK	814
Db	771 LAKNADLHSGTELIVDNS--MAPASDIALPLETKVATVPIDK	811

## RESULT 8

```

US-09-541-782-6
; Sequence 6, Application US/09541782
; Patent No. 6284480
; GENERAL INFORMATION:
; APPLICANT: Nislow, Corey
; APPLICANT: Sakowicz, Roman
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Antifungal Assay
; FILE REFERENCE: 1015
; CURRENT APPLICATION NUMBER: US/09/541,782
; CURRENT FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1073
; TYPE: PRT
; ORGANISM: S.pombe
US-09-541-782-6

```

Query Match	3.4%;	Score 145.5;	DB 4;	Length 1073;
Best Local Similarity	18.6%;	Pred. No. 0.024;		
Matches 182;	Conservative 136;	Mismatches 357;	Indels 301;	Gaps 41;

OY	43	GKQATOKTENTLPDEVSKREGINAE-----QIVIKI--TDQGYVTSHGDIHYHYN	90
		:     : :   :   :   :	
Db	147	GQTGTGKTYTMSGD-LSDSDGILSEGAGLIPRALYQLFSSLNDSNOEYAVK-CSYYELYN	204
OY	91	GKVYPDAIISEELLMKDPNYKKLDED----IVNEVKGGYVIKVDCKYYVYLKDAAHADN	145
		: :   :       :   : : :       : : :   :	
Db	205	EEl-RDLLVSEEL--RKPAREFEDTSRRGNVVITGIEESY-INKAGDGLRLREGSHRRQ	260
OY	146	VRTKEEINROKOEHs-----QHREGTPRNDGAVALARSQGRYTDDGIYFNASDIIEDT	200
		: : :   :   :   : :   :   :   :	
Db	261	VAATKCNDLSSRSHSIFTTLHRKVSSGMDETNSLTINN-----NSDDLr--	307
OY	201	GDAYIVPHGDHYHIPKNELsASELAEAFLSGRNLSNRT-----	243
Db	308	-----ASKLMHVDLAGEINI--GRSGAENKRARETGMINOSLTLIGRYI	349
OY	244	-----YR-----RQNSDNTSPRTNWVPVSNPCTTNNTSNNSTNSQASQS	284
		: : : :   :   :   :   :   :   :	
Db	350	NALVEKAHHIPRESKLTIRLLQDSLGRKTKTSMIVTVS--STNTNLREETISTLEAYARA	406
OY	285	NDIDSLLKOLYKLPLSORHVESDGLVFDPAQI---TSRTARGAAVPHGDHYHFIPYSQ	339
		: :   :       :   : :   :   :   :   :	
Db	407	K---SIRNKPPQNQLYFRKVLIKDLVLDIERLNKDNLNATRKKNGYLAESTYKELMDRVQ	463
OY	340	MSEL---EERIARITPLRYRSNHWWPDRPEQPSPQTPPEPSGPQAPANLKI-----	389
		:   :   : :   :   :   :   :   :   :	
Db	464	NKDILLCOEQARKLEVLDLNVKS-----SRQLOLYVSKSNQEHKKEVEALOQLVNSSTE	517
OY	390	-----DSNSSLVSQLVRKVGEGYVFEEEKGISRYVFAKDLPLSETYKNLESKLSKOESVSH	444
		: :       : :   :   :   :   :   :   :	
Db	518	LESYKSENELKLNELVLEIEKRKKKETNEAKITTVAATDLSQYIRESKEYIASLYEKLDRT	577
OY	445	LTAKKENVAPRDQEEFYDKAYNLL-----TEAH	471
		: : :       : :   :   :   :   :	
Db	578	ERNNKEN---ENNFWMLKFNLTLMRSPHGSFTDETNGYFTLLDNFNASMEE LLNTHSN	633
OY	472	KALFENKGRNSDFQALDKLER-----LNDESTINKELVDDLAF LAPIT	516
		:   :       : : : :   :   :   :   :   :	
Db	634	QLITSMTKITEHFQSIDALQASARRSCCAVPNSSIDLIVSELKDSKNSLLDALEHSLODIS	693
OY	517	-HBERLGKPNs-----QIEYTEDE-----VR-IAQL	540
		: :       : : :   :   :   :   :   :   :	
Db	694	MSsOKlGNGlssELLEOKDMKESYROLVOELTRSLYNLOHTHEESOKELMYGVARNIDIAL	753

QY	541	ADKYTTS--DGYIFDEHDIISDEGDAYVTPHMGSHWIGKDSLSDEKVAQAAYTKKGI	598
Db	754	VKTCTTSLNDADII-LSDYISDQKSKFESKQOQDLIANIGKIVSNFLQONESLYTK----	808
QY	599	LPSPDADVKANPTGDSAAAI--YNRVKGEKRIPLVR-----LPMVENTVEYK	645
		: :   :   :   :   :   :   :	
Db	809	-----ADILSHLNDTNSNIRKANEIMNNRSEEFIRMAASQAEIVGANKERIOKTVE--	860
QY	646	NGNLIIPHKDH-YHNIKFAWFDDHTYKAPNG-----YTLLEDLFIATIKUYVEHPDERP	696
		: :   :   :   :   :   :   :	
Db	861	NGSOLLDSKSKAIHSNSRSMDHCLALAESQKQGVNLEVQYTLDRLLQKVK-----E	911
QY	697	HSNDGWMGNASEHVLGKKDHSEDPBKNKFKADEPVEETPAPEYVQVETEKVEAQLKEAEV	756
		: :   :   :   :   :   :   :	
Db	912	HSEDNTRKEKHQQLLDLLESIVGNNDNL-----IDSIKTPHTELQ-----	950
QY	757	LIAKVTDSSLK-----ANATEIAGLRN-----NLTQIMDNNSIIMAA-----EKL	800
		- :   :               :   :   :   :	
Db	951	---KITDHYLKGTTSLANHTNELLGDESLCNLETTIEDTSLVKLETTGDTPSKRELPA	1007
QY	801	LLKGSNPSSVSKKIN	816
		:    :	
Db	1008	TPSWTRDSSLIKETT	1023

## RESULT 9

```

US-09-723-820-6
; Sequence 6, Application US/09723820
; Patent No. 6468760
; GENERAL INFORMATION:
; APPLICANT: Nislow, Corey
; APPLICANT: Sakowicz, Roman
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Antifungal Assay
; FILE REFERENCE: 1015
; CURRENT APPLICATION NUMBER: US/09/723,820
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/541,782
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1073
; TYPE: PRT
; ORGANISM: S.pombe
US-09-723-820-6

```

Query Match	3.4%;	Score 145.5;	DB 4;	Length 1073;
Best Local Similarity	18.6%;	Pred. No. 0.024;		
Matches 182;	Conservative 136;	Mismatches 357;	Indels 301;	Gaps 41;

QY	43	GKQATQKTEMLTPPEVSKREGINAE-----QIVIKI--TDQGYVISHGDHYHYHN	90
		:       :   :   :       :   :	
Db	147	GQTGTGKTYTMSGD-LSDSDGILSEGAGILPRALYQLFSSLDNSNOEYAVK-CSYIELYN	204
QY	91	GKVPYDAIIEELMKDPNYKLKDED-----IVNEVGKGYVIKVDGKXYVYLKDAHADN	145
		:   :         :     : :               : : :	
Db	205	EEL-RDLVSEEL--RKPARVFEDTSRRGNVITGIEESY-IKNAGDGLRLREGSHRQ	260
QY	146	VRTKEEINROKOEHS-----QHREGGTPRNDCAVALARSQGRYTTDDGIIFNASDIEDT	200
		:   :   :           :     :       :   :	
Db	261	VAAATKCNDLSSRSHSIFTTLHRKVSSGMDTETNSLTINN-----NSDDLRL--	307
QY	201	GDAYIVPHGDHYHIPKNELASASELAAEAFELSGRNLNSRT-----	243
		: :     :     :	
Db	308	-----ASKLHMVDLAGSENI--GRSGAENKRARETGMINQSLTLGRVI	349
QY	244	-----YR-----RQNSDNTSRTNVPSVSNPGTTNTNTSNNSTNSQASQS	284
		:   : :   :       :           : : :	
Db	350	NALVEKAHHIYRESKLTRLLODSLGGKTKTSMIVTYS---STNTNLEETISTLEYAARA	406
QY	285	NDIDSLLKQLYKLPLSQRHVESDGLVFEDPAQT-----TSRTARGVAVPHGDHYHFIPIYSQ	339

Db 407 K---SIRNKPQNNQVVERKVLKIDVLDIRKNDLNATRRKKNVYLAESTYKELMDRVQ 463  
QY 340 MSEL---EERARIIPLRYSNHWVPDSRPEQSPQPTPEPSGPQAPNLKI----- 389  
Db 464 NKDLQEQARKLEVLDLNVKS-----SREQLQYVSKSNQEHKKEVEALQQLVNSSTE 517  
QY 390 ----DSNSSLVSQLVRKVGEGYVFEKISRYVEFAKDLPESEYKNEESKLSKQESVSH 444  
Db 518 LESVKSSENEKLEKNEVLVEIEKRKKYETNAKITTVATDLQYRESKEYIASLYEKLDRT 577  
QY 445 LTAKKENVAPRQEFYDKAYNLL-----TEAH 471  
Db 578 ERNNKEN---ENNFWNLKFNLLTMLSFGHSFTDETNGYFTLLDNFNASMEELLNTHSN 633  
QY 472 KALFENKGRNSDFQALDKLLER-----LNDESTNKEKLVDDLAFIAPIT 516  
Db 634 QLLISMKTTEHFQSLDEALQASRSCAVPNSSLDLIVSELKDSKNSLDALEHSLQDIS 693  
QY 517 -HPERLGKPN-----QIEYTEDE-----VR-IAQL 540  
Db 694 MSSQKLNGISSELLIELQDKMESRYQLVQLRSLYNLQHTHESQKELMYGVARNIDAL 753  
QY 541 ADKYTTS--DGIIFDEHDIISDEGDAYVTPHMGSHWIGKDSLSDKEKVAQAAYTKKGI 598  
Db 754 VKTCTSLNDADI--LSDYISDQSKFESKQOOLIANIGKIVSNFLQEQNESLYTK---- 808  
QY 599 LPPSPDADYKANPTGDSAAAI--YNRVKGKRIPLVR-----LPYMEHTVEYK 645  
Db 809 -----ADILHSLNDTNSIRKANEMNNRSEEFLRNAAEQAEIVGANKERIQKTYE-- 860  
QY 646 NGNLIIPKDH-YHNKFAWFDHTYKAPNG-----YLEDLFATIKYVEHPDERP 696  
Db 861 NGSQILDSKSKAISNSRSMYDHCIALAESQKQGVNLEVQTLDRLLQKV-----E 911  
QY 697 HSNQGWGNASEHVLGKKDHSEDPNKNFKADEPVEETPAPEVPQVETEKVEAQLKEAEV 756  
Db 912 HSEDNTEKHKQLLDLLESLGVNNDNL-----IDSIKTPHTELQ----- 950  
QY 757 LLAKYVDSLSK-----ANATETLAGLRN-----NLTIQIMNNSIMAAE-----EKLLA 800  
Db 951 ---KITDHYLKGTTSLANHTNELGLGDESLCNLETTIEDTSLVKLETGTGTPSKRELPA 1007  
QY 801 LLKGSNPSVSKKIN 816  
Db 1008 TSPWTRDSSLIKETT 1023

RESULT 10  
US-08-961-083-118  
; Sequence 118, Application US/08961083  
; Patent No. 6159469  
; GENERAL INFORMATION:  
; APPLICANT: Choi et. al.  
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
; NUMBER OF SEQUENCES: 452  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961,083  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PB340P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 118:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1040 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-961-083-118

Query Match 3.4%; Score 144; DB 4; Length 1040;  
Best Local Similarity 19.2%; Pred. No. 0.03;  
Matches 154; Conservative 111; Mismatches 284; Indels 252; Gaps 38;

QY 127 IKVDGKYV-YLKDAHADNVRTKEEINROKQESHQREGGTPRND-----G 172  
Db 76 LKEGYQYIGYIK-TRKQDNTELSRTVDGKYSARDQSPNSTKTSVYHSAADLEWNOGG 134  
QY 173 AVALARSQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHIPKNELSASELAEEAFL 232  
Db 135 KVSU---QGEASGDDG-----LSEKSSIAADNLSSNSDFA 166  
QY 233 SGRGNLSNRTYRQNSDNTSRTNWVPSVSNPGTNTNTSNNSTNSQASQSDIDSLK 292  
Db 167 S-----QVEQNDHKGESVVRPTVEQGNPVSATTVQSAEEVLAATTND-----R 211  
QY 293 QLYKLPLSQRHVESDG-----LVF-----DPAQITS 318  
Db 212 PEYKLPLETGTQEPHGEAAVREDLPVYTKPLETKGTQPGHEGAAREEPAYTER 271  
QY 319 RTARGVAVPHGDHYHPTPYQSOMSELEERARIIPLRYSNHWVPDSRPEQSPQTPPEPS 378  
Db 272 LATKGTQEPGHE-----GKATVRETELEYTEPVATKGT---QEPHEGERXVEEEL 319  
QY 379 PGPQPA-----PNL-----KIDSNSSLVSQLVR---KVGEGYVFE 411  
Db 320 PALEVTRNRTEIONIPYTTETIOPDPLKNNRRIERQOAGTRTIOEDYIVNGNVET 379  
QY 412 KGISRYVEAKDLSETVKNLESKLSKQESVSHTLTAKKENVAPRQEFYDKAYNLL--TE 469  
Db 380 KEVSRTVA--PYNEVVKVGTLVKVKPVEITNLTKVEN-----KKSITVSYNLIDTTS 431  
QY 470 AHKALFENKGRNSDFQALDKLLERLNDESTNKEKLVDDLAFIAPIT--TH-PERLGKPN 525  
Db 432 AYVS-----AKTOVEHG-DKLVKVEVDIENPAKEQVIG-LDYIPTYTVKTHLTYNLGENN 484  
QY 526 SQIEYTEDEVRIAQLADKYTTSQGIIFDEHDIISDEGDAYVTPHMGSHWIGKDSLSDKE 585  
Db 485 E--ENTETSTQDFQL--EYKKIEIKDIDSVELYKENDRY-----RRYL--SLSEAP 530  
QY 586 KVAQAAYTKKGIPLPSPDADYKANPTGDSAAAIYNRVKGKRIPLVRLPYMEHT---- 641  
Db 531 TDTAKYFVKYK-----SDREKEMLYPVKS-----ITENTDGTY 563  
QY 642 -VEVKNGLIIPHKDHYHNKFAWFDHTY-----KAPNGYT-LEDLFATIK-----Y 687  
Db 564 KTVVAVDQLVEEGTDGK-----DDYFTVAKSKAEQPGVYTSFKQLVTAMQSNISGV 616  
QY 688 YVEHPDERHSNDGWNASEHVLGKKDHS-----EDPNKNFKADE--EPVEET 733  
Db 617 YTLASDM-----TADEVSLGDKQTSYLTGAFTGSLIGSDGTKSYAIYDLKPLFDY 667  
QY 734 PAPEVPQVETEKVEAQLKEAEVLLAKVTSSSL-----KANATETLAGLRNNLTLOI 785  
Db 668 LMGATVREDLIKTVSADSADKENVAALAKAANSANINNVAVEGKISGAKSVAGLVASATNTV 727



QY 786 MDNNSIMAEKLLALKGSN 806  
:1:1 :1:1  
Db 728 IENSSFTG--KLIANHQDSN 745

## RESULT 11

US-09-816-703A-2  
: Sequence 2, Application US/09816703A  
: Patent No. 6455026  
: GENERAL INFORMATION:  
: APPLICANT: Melcher, Thorsten  
: APPLICANT: Mueller, Sabine  
: APPLICANT: Chin, Daniel  
: TITLE OF INVENTION: Use of Protein Tyrosine Phosphatase Zeta as a Biomolecular Target  
: TITLE OF INVENTION: Treatment and Visualization of Brain Tumors  
: FILE REFERENCE: 262/235 AGY  
: CURRENT APPLICATION NUMBER: US/09/816,703A  
: CURRENT FILING DATE: 2001-03-23  
: NUMBER OF SEQ ID NOS: 2  
: SOFTWARE: PatentIn version 3.0  
: SEQ ID NO 2  
: LENGTH: 2314  
: TYPE: PRT  
: ORGANISM: Homo sapiens  
: FEATURE:  
: NAME/KEY: Reference  
: LOCATION: (1)..(2314)  
: OTHER INFORMATION: Krueger, N.X. and Saito, H.: A human transmembrane protein-tyrosi  
: OTHER INFORMATION: ne-phosphatase, PTP zeta, is expressed in brain and has an N-term  
: OTHER INFORMATION: Inal receptor domain homologous to carbonic anhydrases; Proc. Nat  
: OTHER INFORMATION: L. Acad. Sci. USA 89 (16), 7417-7421 (1992  
: NAME/KEY: Reference  
: LOCATION: (1)..(2314)  
: OTHER INFORMATION: Levy, J.B., et al.: The cloning of a receptor-type protein tyrosi  
: OTHER INFORMATION: ne phosphatase expressed in the central nervous system; J. Biol.  
: OTHER INFORMATION: Chem. 268 (14), 10573-10581 (1993  
: NAME/KEY: SIGNAL  
: LOCATION: (1)..(24)  
: OTHER INFORMATION: By similarity  
: NAME/KEY: DOMAIN  
: LOCATION: (25)..(1635)  
: OTHER INFORMATION: Extracellular (potential)  
: NAME/KEY: misc\_feature  
: LOCATION: (25)..(2314)  
: OTHER INFORMATION: Mature chain; protein-tyrosine phosphatase zeta  
: NAME/KEY: DOMAIN  
: LOCATION: (34)..(302)  
: OTHER INFORMATION: Carbonic-anhydrase like  
: NAME/KEY: SITE  
: LOCATION: (105)..(105)  
: OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)  
: NAME/KEY: SITE  
: LOCATION: (134)..(134)  
: OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)  
: NAME/KEY: SITE  
: LOCATION: (223)..(223)  
: OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)  
: NAME/KEY: SITE  
: LOCATION: (232)..(232)  
: OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)  
: NAME/KEY: DOMAIN  
: LOCATION: (312)..(406)  
: OTHER INFORMATION: Fibronectin Type-III  
: NAME/KEY: SITE  
: LOCATION: (324)..(324)  
: OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)  
: NAME/KEY: SITE  
: LOCATION: (381)..(381)  
: OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)  
: NAME/KEY: SITE  
: LOCATION: (497)..(497)  
: OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)  
: OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)

: NAME/KEY: SITE  
: LOCATION: (501)..(501)  
: OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)  
: NAME/KEY: SITE  
: LOCATION: (552)..(552)  
: OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)  
: NAME/KEY: BINDING  
: LOCATION: (587)..(587)  
: OTHER INFORMATION: Chondroitin sulfate (potential)  
: NAME/KEY: SITE  
: LOCATION: (602)..(602)  
: OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)  
: NAME/KEY: SITE  
: LOCATION: (629)..(629)  
: OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)  
: NAME/KEY: BINDING  
: LOCATION: (637)..(637)  
: OTHER INFORMATION: Chondroitin sulfate (potential)  
: NAME/KEY: SITE  
: LOCATION: (677)..(677)  
: OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)  
: NAME/KEY: VARSPLIC  
: LOCATION: (755)..(1614)  
: OTHER INFORMATION: Splicing variant; missing (in short isoform)  
: NAME/KEY: BINDING  
: LOCATION: (997)..(997)  
: OTHER INFORMATION: Chondroitin sulfate (potential)  
: NAME/KEY: SITE  
: LOCATION: (1017)..(1017)  
: OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)  
: NAME/KEY: SITE  
: LOCATION: (1050)..(1050)  
: OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)  
: NAME/KEY: SITE  
: LOCATION: (1082)..(1082)  
: OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)  
: NAME/KEY: SITE  
: LOCATION: (1122)..(1122)  
: OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)  
: NAME/KEY: SITE  
: LOCATION: (1456)..(1456)  
: OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)  
: NAME/KEY: BINDING  
: LOCATION: (1548)..(1548)  
: OTHER INFORMATION: Chondroitin sulfate (potential)  
: NAME/KEY: BINDING  
: LOCATION: (1550)..(1550)  
: OTHER INFORMATION: Chondroitin sulfate (potential)  
: NAME/KEY: SITE  
: LOCATION: (1561)..(1561)  
: OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)  
: NAME/KEY: SITE  
: LOCATION: (1617)..(1617)  
: OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)  
: NAME/KEY: TRANSMEM  
: LOCATION: (1636)..(1661)  
: OTHER INFORMATION: Transmembrane region; potential  
: NAME/KEY: DOMAIN  
: LOCATION: (1662)..(2314)  
: OTHER INFORMATION: Cytoplasmic (potential)  
: NAME/KEY: CONFLICT  
: LOCATION: (1722)..(1728)  
: OTHER INFORMATION: Missing (in ref. 2)  
: NAME/KEY: DOMAIN  
: LOCATION: (1744)..(1997)  
: OTHER INFORMATION: Protein-tyrosine phosphatase  
: NAME/KEY: ACT\_SITE  
: LOCATION: (1932)..(1932)  
: OTHER INFORMATION: Active site; by similarity  
: NAME/KEY: DOMAIN  
: LOCATION: (1998)..(2314)  
: OTHER INFORMATION: Protein-tyrosine phosphatase  
: NAME/KEY: misc\_feature





Db 863 VTVP-VEILSTDARTHSLDNR-----SQDSPGESEETL--RLTESDSV 902  
QY 442 -SHTLTAKKENAVPR---DOEFYKAYNLLTEAHKALFENKGRNSDFQALDK----- 489  
Db 903 LADDILASRVSVGSSLPGLQELHNKPFSEDDHSHRLEKNLEAVETLNQLNSKDAAKEA 962  
QY 490 -LLERLNDESTNKEKLVDDLAFAPITHPERLGKPNISQIEYTEDEVRIAQLADKYTTSD 548  
Db 963 GLVSALSSDSSTQSQSLLEDLSAPFPASEPS-LETSPD-LESV----- 1003  
QY 549 GYIFDEHDIISDEGDAYVTPPHMGSHWIGKDSLDEKVAQAAYTKE-----KGILPPSP 603  
Db 1004 ---DVHEALLDSLGSHTP-----QKLVPPDKPADSGYETENLESPEWTLHPAP 1048  
QY 604 DADVKANP--TGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEYKNGNLIIPHKDHYHNK 661  
Db 1049 EGTADSEPATGDSGHS-----GLPENPVI---VISDAGDGHGTEVTP----- 1089  
QY 662 FAWFDHTYKAPNGYTLLEDLFATIKYVEHPDERPHSNDGNGNASEHVLGKKDHSEDPNK 721  
Db 1090 -----ETFTAGSQSGSYRD-----SAVFSNDSEPEKR-----SEEVPG-----TSPSA 1127  
QY 722 NFKADEEPEVEETPAEPEVPQVETEKVEAQLKEAE--VLLAKYTDSSLKANAT 771  
Db 1128 LVLVQEOPLPEPVLPEOSPAQDSCLEARKSQPDESCLALHNSSDLELRAT 1179

## RESULT 13

US-07-920-281C-2  
; Sequence 2, Application US/07920281C  
; Patent No. 5739026  
; GENERAL INFORMATION:  
; APPLICANT: Garoff, Henrik  
; APPLICANT: Liljestrom, Peter  
; TITLE OF INVENTION: DNA Expression Systems Based on  
; TITLE OF INVENTION: Alphaviruses  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch  
; STREET: P.O. Box 747  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/920,281C  
; FILING DATE: 13-AUG-1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murphy Jr., Gerald M.  
; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 828-103P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-241-1300  
; TELEFAX: 703-241-2848  
; TELEX: 248345  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2431 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-07-920-281C-2

Query Match 3.3%; Score 140; DB 1; Length 2431;  
Best Local Similarity 19.7%; Pred. No. 0.23;  
Matches 137; Conservative 93; Mismatches 253; Indels 212; Gaps 34;

QY 76 QGVYTSBGDHYHYNG-KVPYDAIISELLMKDPNKLKDEDIVNEVKGGVYIKVDGKY 134  
Db 1523 KGVSTTDGSLSYFEETGTFNQAAIDMAEILLMPRLQEANEOICLYALGETM----- 1574  
QY 135 VYLKDAHADNVRTKEEINROKQEHSHREGGTPRNDGAVALARSGRYTTDDGYIFNAS 194  
Db 1575 -----DNIRSKCPVN-----DSDSTPRT-VPCLCR-----YAMTAE 1606  
QY 195 DIEDTG-----DAIVPHGDHYHYIPKNLSASELAEEAFISGRGNLSNRTYR 245  
Db 1607 RIARLRSHQVKSMVYCSSFPLP---KYHVDGQVKCKEYVLLFDPYV---SVSPRKYA 1660  
QY 246 RQNSDNTSRT-----NWVPSVSNPGTTNTNTSNNSTNSQASQSDIDSLKQLYKPL 299  
Db 1661 ASTTDHSDRSRLRGFDLW-----TTDSSSTASDTMSLPSLQSCDIDSIEYPMPIV 1712  
QY 300 -SQRHVESDGLVEDPAQITRTARGVAVPHGDHYHFIPYSQMSLEERARIIPLRYSN 358  
Db 1713 TADVHPEPAGIADLAADVHPEPA-----DHV-----DLENPIP---PPRPKRA 1752  
QY 359 HWVPDSRPEQSPQPTPEPSPGPQAPAPNKT-----DSNSSLVSQIVRKVGEGVFEKG 413  
Db 1753 AYLASRAAERPVPAPR-KPTPAPRTAFRNKLP/LTEGDFDEHEVDALASGITFGDFDVL 1811  
QY 414 ISR---YVFAKDLBSETVKNLESKLSKQESVSHLLTAKKENAVAPRDQEFYDKAYNLTFA 470  
Db 1812 LGRAGAYIFFSDTGS---GHLQOKSVRQ-----HNLQCAQLDAVQEEKMPPK---LDTER 1861  
QY 471 HKALF-----ENKGRNSDFQALDKLERLNDESTNKEKLVDDLAFAP---ITHP 518  
Db 1862 EKLILLKMQMHPSEANKSRYS-QS-RKVENMKATVVDRLTSGARLYTGADVGRIPTYAVR 1920  
QY 519 ERLGKPNISQIEYTEDEVRIA---QLADKYTSDGY-IFDEHDIISDEGDAYVTPPHMGS 573  
Db 1921 RPVYSPTVIERFSSPDVAIAACNEYLSRNPVTVAASYQITDEYDAYLDMVD----- 1970  
QY 574 HWIGKDSLSDKE---KVAQAAYTKEKGI-----LPPSP-----DADVKAN----- 610  
Db 1971 ---GSDSCLDRATFCRAKLCRCYPKHHAHQPTVRSVAVSPFQNTLQNLVLAATKRNCAVT 2027  
QY 611 -----PTGDSAAAIYN-----RVGKEKR--- 628  
Db 2028 QMRELPTMS--AVFNVECFKRYACSGEYWEYAKOPIRITTENTITTYTKLKGPKAAL 2085  
QY 629 -----IPLVRLPYMVEHTVEYKNGNLIIPKDH 656  
Db 2086 FAKTHNLVPLQVVP-MDRFTVDMKRDVKYTPGTKH 2119

## RESULT 14

US-08-466-277-2  
; Sequence 2, Application US/08466277  
; Patent No. 6190666  
; GENERAL INFORMATION:  
; APPLICANT: Garoff, Henrik  
; APPLICANT: Liljestrom, Peter  
; TITLE OF INVENTION: DNA Expression Systems Based on  
; TITLE OF INVENTION: Alphaviruses  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch  
; STREET: P.O. Box 747  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,277

FILING DATE: 06-Jun-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/920,281  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy Jr., Gerald M.  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 828-103P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-241-1300  
TELEFAX: 703-241-2848  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2431 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-08-466-277-2

Query Match 3.3%; Score 140; DB 4; Length 2431;  
Best Local Similarity 19.7%; Pred. No. 0.23;  
Matches 137; Conservative 93; Mismatches 253; Indels 212; Gaps 34;

QY 76 QGYVSHGDHYHYNG-KVPYDAIISELLMKDPNYKDKEDIVNEVKGGYVTKVDGKYY 134  
Db 1523 KGYSTDDGSLSYFEGTKFNOAIDMAEILTLWPRLOEANEQICLYALGETM----- 1574  
QY 135 VYLKDAHADNVRTKEEINROKOEHSQHREGGTPRNDGAVALARSGRYTTDDGYIFNAS 194  
Db 1575 -----DNIRSKCPVN-----DSDSSTPRT-VPCLCR-----YAMTAE 1606  
QY 195 DIEDTG-----DAIVPHGDHYHYIPKNEISASELAFAFLSGRGNLSNRTYR 245  
Db 1607 RIARLRSHOVKSMVVCSPFLP--KYHVDGVQKCEKVLLEDPVTP--SVSPRKYA 1660  
QY 246 RONSNDTSRT-----NWVPSVSNPGTTNTNTSNTNSQASQSDIDSILKQLYKLP 299  
Db 1661 ASTTDSRSLRGLFDLW-----TTDSSSTASDTMSLPSLQSCDIDSIEPMAPIVV 1712  
QY 300 -SQRHVESDGLVFDPQAQITSRTARGVAVPHGDHYHFIPIYSQMSLEERARIILRYRSN 358  
Db 1713 TADVHPERAGIADLADVHERA-----DHV-----DLENPFP--PPRPKRA 1752  
QY 359 HWVPDSRPEQSPPTPEPSPGPAPAPNLKI-----DSNSSLVSQLVKRVGEGYVFEKEG 413  
Db 1753 AYLASRAERPVAPR-KPTPARTRAFRNKLPITFGDFDEHEVDALASGITFGDFDVL 1811  
QY 414 ISR---YVFAKDLPESETVKNLESKLSKQESVSHLTAKKENVAPRDOEFYDKAYNLTEA 470  
Db 1812 LGRAGAYIFSSDTGS---GHLQKQSVRQ---HNLQCAQLDAVQEEKMTPPK---LDTER 1861  
QY 471 HKALF-----ENKGRNSDFQALDKLLERLNDESTNKEKLVDDLAFAP---ITHP 518  
Db 1862 EKLLLLKMQMHPSEANKSRYSQ--RKEVENKATVVDRLTSGARLYTGADVGRIPYAVRYP 1920  
QY 519 ERLGKPNQIEYTEDEVRIA---QLADKYTTSQGY-IFDEHDIISDEGDAYVTPHMGHS 573  
Db 1921 RPVYSPTVIERSSPDVAIAACNEYSRNYPTVASYQITDEXDAYLDMVD----- 1970  
QY 574 HWIGKDSLDEK---KVAQAAYTKEKGI-----LPPSP-----DADVKAN----- 610  
Db 1971 ---GSDSCLDRATFCPAKLRCPKHAHYHQPTVRSAPVSPFQNTLQNVLAATKRCNCNT 2027  
QY 611 -----PTGSAAIYN-----RVKGEKR--- 628  
Db 2028 QMRELPTMDS--AVFNVECFKRYACSGEYWEYAKQPIRITTEENITTYVTKLKGPKAAL 2085  
QY 629 -----IPVLRLPYMVEHTVEVKNGLIIPHKDH 656  
Db 2086 FAKTHNLVPLQEVF-MDRFTVDMKRDVKVTPTGTXH 2119

RESULT 15  
US-09-513-783A-22  
Sequence 22, Application US/09513783A  
Patent No. 6416959  
GENERAL INFORMATION:  
APPLICANT: Giuliano, Kenneth A.  
APPLICANT: Kapur, Ravi  
TITLE OF INVENTION: A System for Cell Based Screening  
FILE REFERENCE: 97-022-L1  
CURRENT APPLICATION NUMBER: US/09/513,783A  
CURRENT FILING DATE: 2000-02-25  
NUMBER OF SEQ ID NOS: 180  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 22  
LENGTH: 1610  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
US-09-513-783A-22

Query Match 3.2%; Score 137.5; DB 4; Length 1610;  
Best Local Similarity 19.8%; Pred. No. 0.19;  
Matches 174; Conservative 103; Mismatches 337; Indels 265; Gaps 41;

QY 73 ITDQY-----VTSBGDHYHYNGKVPYDAIISELLMKDP-NYKDKDE-----DIY 118  
Db 62 VTTFGYGLQCFARYPDHMKQHDFKSAPEGYVQERTIFPKDGNKYTRAEVKFEGLTLV 121  
QY 119 NEVK-GGYVTKVDG-----KYVYLKDAHADNVRTKEEINROKOEHS---Q 161  
Db 122 NRIELKIDPEKEDGNILGHKLEYNYSNHNVIYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181  
QY 162 HREGGTPRNDGAV-----ALARSQ-----RYTTDDGY-----IFNAS 194  
Db 182 HYQNTPIGDGPVLLPDNHYLSQASALSKDPNEKRDMVLEFVTAAGITLGMDELYKKG 241  
QY 195 DIEDTGDAYIVPHGDHYHYIP--KNELSASELAFA-----FLS 233  
Db 242 DEVDMADLSLV--DALTEPPEIEGEIKRDFMALEAEPPYDDIVGETVEKTEFIPLLD 298  
QY 234 GRGNLSNRTYRONSNDTSRTMWVPSVSNPGTTNTNTSNTNSQASQSDIDSILKQ 293  
Db 299 GDEKGTGSESKKKPCLD-TSQVEGIPS-SKP-TLLANGDHGMEGNNTAGSPITD---FLEE 352  
QY 294 LYKLP---LSQRHVESDGLVFDPQAQITSRTARGVAVPHGDHYHFIPIYSQMSLEERARI 350  
Db 353 RVDYPDYQSSQNWNPEDASFQCPQOVLDTQ---AEFPNEH-----RDDGLADL 398  
QY 351 IPLRYSNHWVPDSRPEQSPPTPEPSPGPAPAPNLKIDSNSLSVQLVKRVGEGYVFE 410  
Db 399 LFVSSGPTNASAFTERDNPS-----EDSYGMLPCDSF---ASTAVVSQEMS VGAPNSPCS 450  
QY 411 EKGISRYVEFAKDLPESETVKNLE---SKLSKQESVSHLTAKKENVAPRDOEFYDKAYN 465  
Db 451 ESCVS-----PEVTIETLQPA TELSKAAEVESVKEQLPAK----- 485  
QY 466 LITEAHKALFENKGRNSDFQALDKLLERLN-----ESTNKEKLVDDLAFAPITHPERL 521  
Db 486 -----ALETMAEQTTDVVHSPSTDTPTGPDTEAALAKDIE----- 520  
QY 522 GKNPSQIEYTEDEVRIAQLADKYTTSQGYIFDEHDIISDEGDAY----- 565  
Db 521 -----EITKPDVILANVTQPTSTESDMFLQDMELLTGEAHAHANNILPTEPDESSTK 573  
QY 566 -VTPHMGHSHWIGKDSLDEKVA---QAYTKEKGLPPSPDADVKANPT 612  
Db 574 DVAPRMEEEIVPGNDTSPKETETLPIKMDLAPPEDVLLTKETELAP---AKGMVSL 629  
QY 613 GDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGLIIPHKDHYNINKEAFWDHTTYKA 672

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Db 630 EIEEALAKNDVRSAE-IPVAQ-ETVSVSETEVVLATEVVL----- 667
QY 673 PNGYTLEDLFATIKYVEHP--DERPHSNDGNGN-ASEHVLGKKD-HSEDPNKNFKADEE 728
Db 668 -----SDPITTLTKDVTLLPLEAERPLVTDMTSPLETEMTLGKETAPPTETNLGMAKDMS 721
QY 729 PVEETPAE-----PEVPQVETEKVEAQKAEVLLAKVTDSSSLKANATETLAGLRNN 780
Db 722 PLPESEVTLGKDVILLPETKVAEFNNV-TPLSEEEV--TSVKDMSPSA---ETEAPLAKN 775
QY 781 LTIQ-----IMDNNSIMAEAKLLALLKGSNPSSVSKEK 814
Db 776 ADLHSGTELIVDNS-MAPASDLALPLETKVATVPIKDK 812
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Search completed: May 19, 2003, 08:25:07  
Job time : 32.7448 secs

GenCore version 5.1.4-p5.4578  
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## OM protein - protein search, using sw model

Run on: May 19, 2003, 07:51:03 ; Search time 234.436 Seconds  
(without alignments)  
335.715 Million cell updates/sec

Title: US-09-645-835A-7

Perfect score: 4265

Sequence: 1 MKINKKYLVGSAALLILSV.....KLLALLKGSNPSSVSKEKIN 816

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

Total number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
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- 12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4163	97.6	796	10	US-09-765-272-56
2	3304	77.5	840	9	US-09-884-465A-7
3	2832.5	66.4	838	9	US-09-884-465A-8
4	2661.5	62.4	763	10	US-09-765-272-66
5	1902	44.6	1126	9	US-09-884-465A-383
6	1894.5	44.4	1365	9	US-09-884-465A-382
7	1798.5	42.2	1139	9	US-09-884-465A-380
8	1798.5	42.2	1378	9	US-09-884-465A-378
9	1668	39.1	1238	9	US-09-884-465A-381
10	1659	38.9	999	9	US-09-884-465A-376
11	1652	38.7	999	9	US-09-884-465A-377
12	1295.5	30.4	1039	9	US-09-884-465A-6
13	1186.5	27.8	447	10	US-09-765-272-182
14	991.5	23.2	913	9	US-09-884-465A-384
15	991.5	23.2	1152	9	US-09-884-465A-379
16	975.5	22.9	840	9	US-09-884-465A-10
17	927	21.7	793	9	US-09-252-088-15
18	724.5	17.0	906	9	US-09-884-465A-369
19	715.5	16.8	906	9	US-09-884-465A-373

20	711.5	16.7	906	9	US-09-884-465A-371	Sequence 371, App
21	676.5	15.9	900	9	US-09-884-465A-333	Sequence 333, App
22	660	15.5	715	9	US-09-252-088-16	Sequence 16, Appl
23	645	15.1	906	9	US-09-884-465A-370	Sequence 370, App
24	645	15.1	906	9	US-09-884-465A-372	Sequence 372, App
25	643	15.1	272	9	US-09-884-465A-258	Sequence 258, App
26	643	15.1	895	9	US-09-884-465A-344	Sequence 344, App
27	643	15.1	901	9	US-09-884-465A-343	Sequence 343, App
28	641	15.0	272	9	US-09-884-465A-300	Sequence 300, App
29	641	15.0	272	9	US-09-884-465A-301	Sequence 301, App
30	636	14.9	894	9	US-09-884-465A-336	Sequence 336, App
31	636	14.9	900	9	US-09-884-465A-335	Sequence 335, App
32	636	14.9	906	9	US-09-884-465A-332	Sequence 332, App
33	634	14.9	272	9	US-09-884-465A-293	Sequence 293, App
34	634	14.9	272	9	US-09-884-465A-294	Sequence 294, App
35	634	14.9	272	9	US-09-884-465A-295	Sequence 295, App
36	627	14.7	894	9	US-09-884-465A-340	Sequence 340, App
37	627	14.7	894	9	US-09-884-465A-342	Sequence 342, App
38	627	14.7	900	9	US-09-884-465A-339	Sequence 339, App
39	627	14.7	900	9	US-09-884-465A-341	Sequence 341, App
40	626	14.7	270	9	US-09-884-465A-302	Sequence 302, App
41	625	14.7	272	9	US-09-884-465A-296	Sequence 296, App
42	625	14.7	272	9	US-09-884-465A-298	Sequence 298, App
43	625	14.7	272	9	US-09-884-465A-299	Sequence 299, App
44	625	14.7	895	9	US-09-884-465A-346	Sequence 346, App
45	625	14.7	901	9	US-09-884-465A-345	Sequence 345, App

## ALIGNMENTS

RESULT 1  
US-09-765-272-56  
Sequence 56, Application US/09765272  
Patent No. US20020061545A1

GENERAL INFORMATION:  
APPLICANT: Choi et. al.  
TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines  
NUMBER OF SEQUENCES: 452  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/765,272  
FILING DATE: 22-Jan-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/961,083  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PB340P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 796 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 56:



US-09-765-272-56

Query Match	97.6%	Score 4163;	DB 10;	Length 796;
Best Local Similarity	99.98%	Pred. No. 8.2e-255;		
Matches 795; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	21	SYELGLYQARTVKENNRVSYIDGKOATQKTENLTPDEYSKREGINAEQIVIKITDOGYVT	80
Db	1	SYELGLYQARTVKENNRVSYIDGKOATQKTENLTPDEYSKREGINAEQIVIKITDOGYVT	60
QY	81	SHGDHYHYXNGKVPYDAIISELLMKDPNYKKLDEDIVNEVKGGYIVKDGKYYVYLKDA	140
Db	61	SHGDHYHYXNGKVPYDAIISELLMKDPNYKKLDEDIVNEVKGGYIVKDGKYYVYLKDA	120
QY	141	AHADNVRTKEEINRQOEHSQHREGTPRNDGAVALARSGRYTTDDGYIFNASDIIEDT	200
Db	121	AHADNVRTKEEINRQOEHSQHREGTPRNDGAVALARSGRYTTDDGYIFNASDIIEDT	180
QY	201	GDAYIVPHGDHYHIYPKNELASASELAAAEAFLSGRGNLSNRTYRRONSDNTSRTNWVPS	260
Db	181	GDAYIVPHGDHYHIYPKNELASASELAAAEAFLSGRGNLSNRTYRRONSDNTSRTNWVPS	240
QY	261	VSNPGTNTNTSNNSNTNSQASQSDIDSLKQLYKPLPSORHVESDGLVFDPAQITTSRT	320
Db	241	VSNPGTNTNTSNNSNTNSQASQSDIDSLKQLYKPLPSORHVESDGLVFDPAQITTSRT	300
QY	321	ARGVAVPHGDHYHFIPIYSQMSSELEERIARIIPLRYSNHVWVDSRPEQSPQPTPEPSPG	380
Db	301	ARGVAVPHGDHYHFIPIYSQMSSELEERIARIIPLRYSNHVWVDSRPEQSPQPTPEPSPG	360
QY	381	POPAPNLKIDNSSLSVSQLVRKVGEGYVFEEEKGISRYVFAKDLPSETVKNLESKLSQES	440
Db	361	POPAPNLKIDNSSLSVSQLVRKVGEGYVFEEEKGISRYVFAKDLPSETVKNLESKLSQES	420
QY	441	VSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFENKGRNSDFQALDKLLERLNDSTN	500
Db	421	VSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFENKGRNSDFQALDKLLERLNDSTN	480
QY	501	KEKLVDDLAFAPLPIHPERLGKPNISOIETEDEVRIAOQLADKYTTSDGYIFDEHDIISD	560
Db	481	KEKLVDDLAFAPLPIHPERLGKPNISOIETEDEVRIAOQLADKYTTSDGYIFDEHDIISD	540
QY	561	EGDAYVTPHMGHSHWIGKDSLSDKEVAAQAYTKEKGILPEPSPDADVKANPTGDSAAAIY	620
Db	541	EGDAYVTPHMGHSHWIGKDSLSDKEVAAQAYTKEKGILPEPSPDADVKANPTGDSAAAIY	600
QY	621	NRVKGGEKRIPVLRPLYMVEHTVEYKNGNLIIPHKHYNHIKFAWFDHTYKAPNGYTLIED	680
Db	601	NRVKGGEKRIPVLRPLYMVEHTVEYKNGNLIIPHKHYNHIKFAWFDHTYKAPNGYTLIED	660
QY	681	LFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSSEDPNKNFKADEEPVEETPAPEPEVP	740
Db	661	LFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSSEDPNKNFKADEEPVEETPAPEPEVP	720
QY	741	QVETEKVEAOQLKEAEVLLAKVTDSSLLKANATETLAGLRNNLTQIMDNNSIMAEAEKLLA	800
Db	721	QVETEKVEAOQLKEAEVLLAKVTDSSLLKANATETLAGLRNNLTQIMDNNSIMAEAEKLLA	780
QY	801	LLKGSNPSSVSKEKIN 816	
Db	781	LLKGSNPSSVSKEKIN 796	

RESULT 2  
US-09-884-465A-7

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; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 840
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-884-465A-7

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Query Match	77.58;	Score 3304;	DB 9;	Length 840;
Best Local Similarity	75.38;	Pred. No. 1.6e-200;		
Matches 632;	Conservative 67;	Mismatches 106;	Indels 34;	Gaps 3;

QY	1	MKINKYLVGSAABLLILSVCSYELGLYQARTVKENNRVSYIDGKQATQKTENLTPEVSK	60
Db	1	MKINKYLVGSAABLLILSVCAVELGLHQAQTVKENNRVSYIDGKQATQKTENLTPEVSK	60
QY	61	REGINAEQIVIKITDQGYVTSHGHDHYHNGKVPYDAIISELLMKDPNYKLKDEIVNE	120
Db	61	REGINAEQIVIKITDQGYVTSHGHDHYHNGKVPYDAIISELLMKDPNYQLKDSIVNE	120
QY	121	VKGYVIVKVDGKYVYVYLKDAHADNVRTKEEINRQKQESHQREGGTPRNDGAVALARQ	180
Db	121	IKGYVIVKVGKYYVYVYLKDAHADNVRTKEEINRQKQESHQREGGTSANDGAVAFARSQ	180
QY	181	GRYTTDDGYIFNASDIIEDTGDAYIVBGHDHYHYPKNELASSELAAAEAFLSGRNLSN	240
Db	181	GRYTTDDGYIFNASDIIEDTGDAYIVBGHDHYHYPKNELASSELAAAEAFLSGRNLSN	240
QY	241	SRTYRRQNSDNTSRTNMVPSVSNPGTTNTNTSNTSNTSQAQSQNDIDSLKLQVLPUS	300
Db	241	LRTYRRQNSDNTSRTNMVPSVSNPGTTNTNTSNTSNTSQAQSQNDIDSLKLQVLPUS	300
QY	301	QRHVESDGLVFEDPAQITSRTARGVAVPHGDHYHFIPIYSQMSLELERIARIIPLRYSNMW	360
Db	301	QRHVESDGLVFEDPAQITSRTARGVAVPHGNHYHFIPIYEQMSLEKRIARIIPLRYSNMW	360
QY	361	VPDSRPEQSPQPTPEPSPGPQAPAPNLK-IDSN--SSLVSQLVKVGEGYVEEEKISR	416
Db	361	VPDSRPEEPSPQPTPEPSPGPQAPAPNPQAPAPNPIDEKLYKAEVKKVGDGVEEENGYSR	420
QY	417	YVEAKDLPSEIVKNLESKLSKQESVSHTLTAKKENVAPRDQEEFYDKAYNLLTEAHKALFE	476
Db	421	YIPAKNLSAETAGIDSKLAKQESLSHKLGAKKTDLPSSDREFFYNKAYDDLARIHQDILLD	480
QY	477	NKGRNSDFQALDKLERLNDESTINKEKLVDDLAFAPITHEBERLGKPNQIEYTEDEVR	536
Db	481	NKGRQVDFEALDNLERLKDVSDDKVKLVDDILAFLAPIRHEBERLGKPNQIITYDDEIQ	540
QY	537	IAQLADKYTTSDSGYIFEHDIISDEGDAYVTPHMGSHWIGKDSLDSKEKVAQAQYTKEK	596
Db	541	VAKLAGKYTTEDEGYIFEDPRDITSDEGAYVTPHMTSHHWIKDLSLSEAERAAQAQYAKEK	600
QY	597	GILPSPDADYKANPTGDSAAAIYNRYKGEKRIPLVRLPYWVEHTVEVKNGNLITPHKDH	656
Db	601	GLTPPSTDHQDSGNTAEAKGAEAIIYNRYKAAKKVPPLDRMPYNLQYTVVEVKNGLIIPHYDH	660
QY	657	YHNKIFAWFEDHTYKAPNGYTTLEDLEFATIKYYVEHPDERPHSNDGWNASEHYLGKDDHS	716
Db	661	YHNKIFEFWFEDEGLYEAPKGYYTLEDLATVKKYYVEHPNERPHSDNGFGNASDHYQRNKNQ	720
QY	717	EDPNKNFKAD-----EEVVEETPAPEVPOVETEK	746
Db	721	ADTNQTEKPSPEEKQOTEKPEEETPREKKPQSEKPESPKPTPEEPEEESPEESEEPQVETEK	780
QY	747	VEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTIQIMDNNSIMAAEKLALLGKS	805

Db 781 VEEKLEAREADLLGKIQDPIIKSNAKETLTGLKNNLFGTQDNNNTIMAEAEKLLALLKES 839

RESULT 3

US-09-884-465A-8  
; Sequence 8, Application US/09884465A  
; Publication No. US20030077293A1

GENERAL INFORMATION:

; APPLICANT: Shire Biochem, Inc.  
; APPLICANT: Hamel, Josee  
; APPLICANT: Brodeur, Bernard  
; APPLICANT: Martin, Denis  
; APPLICANT: Charland, Nathalie  
; APPLICANT: Ouellet, Catherine  
; TITLE OF INVENTION: Streptococcus Antigens  
; FILE REFERENCE: 055190-0044  
; CURRENT APPLICATION NUMBER: US/09/884,465A  
; PRIOR FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: 60/212,683  
; NUMBER OF SEQ ID NOS: 384  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 838  
; TYPE: PR  
; ORGANISM: Streptococcus pneumoniae  
US-09-884-465A-8

Query Match 66.4%; Score 2832.5; DB 9; Length 838;  
Best Local Similarity 64.9%; Pred. No. 9.5e-171;  
Matches 554; Conservative 91; Mismatches 148; Indels 61; Gaps 8;

QY 1 MKINKYLVGSAALILSVCSYELGLYQARTV-KENNRVSYIDGQATOKTENTPDEV 59  
Db 1 MKINKYLVGSAALILSVCSYELGLYQARTV-KENNRVSYIDGQATOKTENTPDEV 59  
QY 60 KREGINAEQIVIKITDQGYVTSHGDIHYHYNGKVPYDAISELLMKDPNYKTKDEIVN 119  
Db 61 KREGINAEQIVIKITDQGYVTSHGDIHYHYNGKVPYDAISELLMKDPNYKTKDEIVN 120  
QY 120 EVKGYVTKVDGKYVYVYLKDAHADNVRTKEEINRQKQESHQHREGTPRNDGAVALLARS 179  
Db 121 EIKGYVTKVDGKYVYVYLKDAHADNVRTKEEINRQKQESHQHREGTPRNDGAVALLARS 177  
QY 180 QGRYTTDDGYIFENASDIETDGAIVPHGDHYHYIPKNEISASELAAEAFLSGRNL 239  
Db 178 QGRYTTDDGYIFENASDIETDGAIVPHGDHYHYIPKNEISASELAAEAFLSGRNL 232  
QY 240 NSRTYRONSNDTSRTNMVPSVSNPGTNTNTSNNSTNSQASQSDNIDSLKQLYKPL 299  
Db 233 -----KQGRSPSSSSSYNANPYQRLSENHNLVTPTYHQ-NQGENISSLLRELYAKPL 285  
QY 300 SQRHVESDGLVEDPAQITSRARGAVPHGDHYHYIPYQMSSELEERARIIPLRYSNH 359  
Db 286 SERHVESDGLIEDPAQITSRARGAVPHGDHYHYIPYQMSSELEERARIIPLRYSNH 345  
QY 360 WVPDSRPEQSPQPTPEPS-----PGQPAPNLKIDSNSLVSQLVRKVGEGYVEEK 413  
Db 346 WVPDSRPEQSPQPTPEPSLOPAPNPQAPSPNPID--EKLKVAVRKVGEGYVEENG 403  
QY 414 ISRYFAKDLBSETVKNLESKLSQESVSHLTAKKENVAPRDQEFYDKAYNLTEAHKA 473  
Db 404 VSRYIPAKDLSETVKNLESKLSQESVSHLTAKKENVAPRDQEFYDKAYNLTEAHKA 463  
QY 474 LFENKGRNSDFQALDKLERLNDSTNKEKLVDDLAFAPITHPERLGKPNQIETED 533  
Db 464 LLDNKGROYDFEVLNLLERLKVSSDKVCLVDILAFAPIRHPERLGKPNQIETED 523  
QY 534 EVRIADLADKYTSDGYIFEDHDIISDEGDAYVTPHMGSHWIGKDSLDEKKAQAAYT 593  
Db 524 EIOVAKLAGKYTTEDGYIFEDPRDITSDEGDAYVTPHMTSHWIKKDSLSEAERAAQAAYA 583  
QY 594 KEKGLPPSPDADVKANPTGDSAAAIYNRVKGEKRIPIVRLPYMVEHTVEVKNGLIIPH 653

Db 584 KEKGLTPSPSTDHODSGNTEAKGAFAIYNRVKAACKVPLDRMPYNIQYTVVEVKNGLIIPH 643  
QY 654 KDHYHNKFAWEDDHTYKAPNGYTTLEDFAFIKYYVEHPDERPHSNDGWNASEHYLGK- 712  
Db 644 YDHYHNKFEWFEDEGLYEAPKGYSLLEDLATVKKYYVEHPNERPHSDNGFCNASDHVRKNK 703  
QY 713 -----KDHE-----DPNKNFKADEEPEETPAE 736  
Db 704 ADQDSKPEDDEKHEDEVSEPTHPESDEKENHAGLNPSADNLYKPSIDTTEETEEAEDTTDE 763  
QY 737 PEVPQVETEKVEAQKAEVLLAKVTDSSLSKANATETLAGLRNNLTQIMDNNSIMAEAE 796  
Db 764 AEIPQVENSVINAKIADAEALLEKVTDPSTIRQAMETLTGLKSSLLGKTDNNNTISAEVD 823  
QY 797 KILALLKGSNPPSV 810  
Db 824 SLALLKESQAPAI 837

RESULT 4

US-09-765-272-66  
; Sequence 66, Application US/09765272  
; Patent No. US20020061545A1

GENERAL INFORMATION:

; APPLICANT: Chol et. al.  
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
; NUMBER OF SEQUENCES: 452  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/765,272

FILING DATE: 22-Jan-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/961,083

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Brookes, A. Anders

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PB340P2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 66:

SEQUENCE CHARACTERISTICS:

LENGTH: 763 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 66:

US-09-765-272-66

Query Match 62.4%; Score 2661.5; DB 10; Length 763;

Best Local Similarity 66.8%; Pred. No. 5.2e-160;

Matches 520; Conservative 78; Mismatches 131; Indels 49; Gaps 8;

QY 20 CSYELGLYQARTV-KENNRVSYIDGQATOKTENTLPDEVSKREGINAEQIVIKITDQGY 78  
Db 1 CSYELGRHQAGQYKESNRVSYIDGQAGQKAENLTPDEVSKREGINAEQVXIKITDQGY 60  
QY 79 VTSHGDIHYHYNGKVPYDAIISELLMKDPNYKTKDEIVNEVKGIVIKVDGKYVYVYLK 138

```
|||||
Db 61 VTSBGDHYHYNGKPYDAIISEELMLKDPNQKLDSDIVNEIKGVYIKVNGKYYVYLK 120
QY 139 DAHADNVRTKEELNRQKQEHSHREGGTPRNDCAVALARSQGRYTTDDGYIFNASDIIE 198
Db 121 DAHADNIRTKKEELRQKQERSHNHNS---RADNAVAARAQGRYTTDDGYIFNASDIIE 177
QY 199 DTGDAYIVPHGDHYHYIPKNELSASELAAEAFLSGRGNLSNRYRRQNSDNTSRITNV 258
Db 178 DTGDAYIVPHGDHYHYIPKNELSASELAAEAAYWNG-----KQGSRPSSSSSYN 226
QY 259 PSVSNPGTNTNTNSNSNTNSQASQSDNDISLKLQYKPLSQRHVESDGLVFDPAQITS 318
Db 227 ANPAQPRLSENHNLVTPTYHQ-NQGENISSLLRELKPLSERHVESDGLIFDPAQITS 285
QY 319 RTARGVAVPHGDHYHYIPYSQMSSELEERARIIPLYRSNHWVPDSRPEQSPQTPPEPS 378
Db 286 RTARGVAVPHGNHYHFIPYEQMSELEKRIARIIPLYRSNHWVPDSRPEQSPQTPPEPS 345
QY 379 PGPQAPNLK-IDSN---SSLVSQLVKRYGEGYVEEEKGISRYVFAKDLPSETVKNLESK 434
Db 346 PSPQAPNPQAPAPSNPIDEKLVKAEVRAKVGQDYVEENGVSRYIPAKDLAETAAGIDSK 405
QY 435 LSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFENKGRNSDFQALDKLERL 494
Db 406 LAKQESLSHKLGAKTDLPSDREFYNKAYDLLARIHQDLLDNKGRQYDFEALDNLLERL 465
QY 495 NDESTNKEKLVDDLAFAPITHPERLGRKPNQIETEDEVRIQDLADKYTTSDGYIFDE 554
Db 466 KDVSXSKVKLVXDILAFAPIRHPERLGRKPNQIETEDQIYVAKLAGKYTTEDGYIFDP 525
QY 555 HDIISDEGDAYVPHMGSHWIGKDSLSKEKVAQAAYTKEKGLPPSPDADVKANPTGD 614
Db 526 RDTSDGDAYVPHMTHSHWIKKDSLSEABRAAAQAYAKEKGLPPSTDHODSGNTEAK 585
QY 615 SAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGLIIPHKDHYHNKFAWEDDHTYKAPN 674
Db 586 GAEAIYNRVKAAKVPDLRMPYNLYQTYVEKNGSLIIPHYDHYHNKFEWFEDEGLYEAPK 645
QY 675 GYTLEDLFATIKYVEHPDERPHSNDGNGNASEHVLGKKDHSSEDPKNKFADEE----- 728
Db 646 GYTLEDLATVKKYVEHPNERPHSDNGFCNASDHYQRNKGADTNGTEKPSSEKQTEK 705
QY 729 PVEET-----PAPEVPQVETEKVEAQLEAEVLLAKVTD 763
Db 706 PEEETPREEKPOSEKPESPKPTPEEPSESEPEQVETEKVEEKLREAEDDLKGIQD 763

RESULT 5
US-09-884-465A-383
; Sequence 383, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 383
; LENGTH: 1126
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
```

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; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa = Methionine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (557)..(557)
; OTHER INFORMATION: Xaa = Glycine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (558)..(558)
; OTHER INFORMATION: Xaa = Proline or nothing
US-09-884-465A-383

Query Match 44.6%; Score 1902; DB 9; Length 1126;
Best Local Similarity 64.9%; Pred. No. 8.5e-112;
Matches 366; Conservative 64; Mismatches 100; Indels 34; Gaps 3;

QY 286 DIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSLEE 345
Db 2 DIDSLLKQLYKLPLSQRHVESDGLIFDPAQITSRTARGVAVPHGNHYHFIPYEQMSELEK 61
QY 346 RIARIIPLYRSNHWVPDSRPEQSPQTPPEPSGPQAPNLK-IDSN---SSLVSQLVK 401
Db 62 RIARIIPLYRSNHWVPDSRPEEPSQPTPEPSGPQAPNPQAPAPSNPIDEKLVKAEVR 121
QY 402 KYGEGYVEEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYD 461
Db 122 KYGDGYVEENGVSRYIPAKNLSAETAAGIDSKLAKQESLSHKLGAKTDLPSDREFYN 181
QY 462 KAVNLLTEAHKALFENKGRNSDFQALDKLERLNDESTNKEKLVDDLAFAPITHPERL 521
Db 182 KAYDLLARIHQDLLDNKGRQYDFEALDNLLERLKDVSSDKVLVDILAFAPIRHPERL 241
QY 522 GKPNQIETEDEVRIQDLADKYTTSDGYIFEDHDIISDEGDAYVPHMGSHWIGKDSL 581
Db 242 GKPNQIETEDQIYVAKLAGKYTTEDGYIFDPDITSDGDAYVPHMTHSHWIKKDSL 301
QY 582 SDKEKVAQAAYTKEKGLPPSPDADVKANPTGDSAAATYNRVKGEKRIPLVRLPYMVEHT 641
Db 302 SEAEKVAQAAYAKEKGLPPSTDHODSGNTEAKGAEAIYNRVKAAKVPDLRMPYNLYQY 361
QY 642 VEYKNGNLIIPHKDHYHNKFAWEDDHTYKAPNGYTLEDLFATIKYVEHPDERPHSNDG 701
Db 362 VEYKNGSLIIPHYDHYHNKFEWFEDEGLYEAPKGYTTLEDLATVKKYVEHPNERPHSDNG 421
QY 702 WGNASEHVLGKKDHSSEDPKNKFADEE-----EEPEVE 731
Db 422 FGNASDHYQRNKGADTNGTEKPSSEKQTEKPEEETPREEKPOSEKPESPKPTPEEP 481
QY 732 ETPAPEVPQVETEKVEAQLEAEVLLAKVTDSSLSKANATETLAGLRNNLTIQIMDNNSI 791
Db 482 ESPEESEEPQVETEKVEEKLREAEDDLKGIQDPIIKSNAKETLTGLKNLLFGTODNNTI 541
QY 792 MAEAEKLLALLKGSNPSSVSKKEI 815
Db 542 MAEAEKLLALLKESKXXDLTEEQI 565

RESULT 6
US-09-884-465A-382
; Sequence 382, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
```





```

US-09-884-465A-378
; Sequence 378, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 378
; LENGTH: 1378
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa = Methionine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (570)..(570)
; OTHER INFORMATION: Xaa = Glycine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (571)..(571)
; OTHER INFORMATION: Xaa = Proline or nothing
US-09-884-465A-378

```

Query Match	42.2%;	Score 1798.5;	DB 9;	Length 1378;
Best Local Similarity	60.7%;	Pred. No. 3.9e-105;		
Matches 345;	Conservative 72;	Mismatches 106;	Indels 45;	Gaps 4;

```
Oy      286 DIDSLLKQLYKLPLSQRHVESDGLVEDPAQITSRTARGVAAPHGDHYHFIPYSQMSELEE    345
       : | |:|::|| ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||::
Db        3 NISSLRLEYAKPLSERHVESDGLIFDPQAQITSRGAVAPFHGNHHYHFIPYEOMSELEK   62
```

```
QY      346 RIARIPLKRYSNHWVPDSRPEQPSPQTPEPS-----PGROPAPNLKIDSNSLSYLSQL   399  
        ||| | | | | | | | | | | | | | | | | | | | | :  
Db      63 RIARITPLKRYSNHWWPDSRPEQSPSPSTPEPSLQPAFPNPQAPASNPID--EKLYKEA   120
```

```
QY 400 VRKVGEGYFEEEKISRYPFAKDLPSFVKNLESKLSKQESVSHLTAKKENVAPRDOEF 459
      ||||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 121 VRKVGEGYFEENGVSRIIPAKDLSETAAGIDSKLAKQESLSHKLGAKKTDLPSSDRF 180
```

```

Qy      460 YDKAYNLLTEAHKALFEKNGRNSDFALDKLLERLNDESTNKEKLVDDLLAFLAPIRIHE 519
      | : | : | | | : | : | | | | | : | : | : | | | | | | | |
Db      181 YNKAYDLLARHODLLDNKGRQVDFEVLVDNLLERLKDVSSDKVKLVDDILAFLAPIRIHE 240

```

```
QY      520  RLGPNSQIETEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPMHGSHWICKD  579
        |||||:| |:|:::|:| ||||| | | ||||| ||||| ||||| ||
DB      241  RLGPNAQIYTTDDDEIQVAKLAGKYTTEDGYIFDPRDITSDEGDAYVTPMHTSHWIKD  300
```

```
Qy 580 SLSDEKEVAAYATKEKGLPPSPDADKANPTGDSAAAIYNRVKGCKRIPLVRLPYWE 639
    ||| : : |||| |||| : ||| | ||||| || : : || : || : :
Db 301 SLSAEERAAOAYAKEKGLTPPSTHDGSCNTEAKGAELIYNRVKAAKKVPPLDRMPYNLQ 360
```

Qy 640 HTVEVKNGLIIPHKDHYHNKFEWEDDHYYKAPNGYTLLEDLFATIKYYVEHPDERPSN 699  
 :|||||:||||| ||||| |::| :||| :||| ||-|||||:|||||:  
 Db 361 YTVEVKNGSLIIPHYDHYHNKFEWDDEGLYEAPKGYSLEDLATVKYYVEHPNERPHSD 420

```

OY      700 DGMGNASEHYLGK-----KDHS-----DPKN 722
      :|:|:|:|:| 1:1|
Db      421 NGFGNASDHYAKNKADQDSKPDEDEKHEDEVSEPTHPESDEKENHAGLNP SADNL YKPST 480

```

QY 723 FKAEDEPVEETPAEPVPOVETEKVEQOLKEAEVLLAKVTDSLSKANATETLAGLRNNLT 782  
: || ||: | | || | : ||: || | | || | ||: ||  
: |

Db 481 TEETEEEAEDTTDEAEI PÖVENSVINAKIADA EALL EKVTDP SİRÖNAMETLTGLKSSLL 540

Oy 783 LÖIMDNNSIMAEAEKLLALLKGSNPSSV 810  
| | | | | : | | | | | : | :  
Db 541 LGTKDNNTISA EYD SLLALLKESÖPAPI 568

RESULT 9  
US-09-88

US-09-884-465A-381  
; Sequence 381, Application US/09884465A  
; Publication No. US20030077293A1

```

? GENERAL INFORMATION:
? APPLICANT: Shire Biochem, Inc.
? APPLICANT: Hamel, Josee
? APPLICANT: Brodeur, Bernard
? APPLICANT: Martin, Denis
? APPLICANT: Charland, Nathalie
? APPLICANT: Ouellet, Catherine
? TITLE OF INVENTION: Streptococcus Antigens
? FILE REFERENCE: 055190-0044
? CURRENT APPLICATION NUMBER: US/09/884,465A
? CURRENT FILING DATE: 2001-06-20
? PRIOR APPLICATION NUMBER: 60/212,683
? PRIOR FILING DATE: 2000-06-20
? NUMBER OF SEQ ID NOS: 384
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 381

```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa = Methionine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (430)..(430)
; OTHER INFORMATION: Xaa = Glycine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (431)..(431)
; OTHER INFORMATION: Xaa = Proline or nothing
;
US-09-884-465A-381

```

Query Match	39.1%;	Score 1668;	DB 9;	Length 1238;
Best Local Similarity	66.5%;	Pred. No. 5.8e-97;		
Matches 314; Conservative	58;	Mismatches 96;	Indels 4;	Gaps 2;

```
QY      286 DIDSLLKQLYKLPLISQRHVESDGLVEDPAQITSRTARGVAVPHGDHYHFIPIYSQMSELEF 345  
        |||||  
Db       2 DIDSLLKQLYKLPLISQRHVESDGLIEDPAQITSRTARGVAVPHGNHHYHFIPYEQMLELK 61
```

```
Qy      346 RIARIPLRYSNMHWVDSRPEQSPQPPTPEPSPGPQAPAPNLK-IDSN---SSLVSQLV R 401
          |||||
Db      62  RIARILPLRYSNMHWVDSRPEEPSPQPPTPEPSPGPQAPAPNPIDKLKYEA VR 121
```

```

Oy      402 KVGEGYVFEEKGJSTRVFEAKDLPSEYVKNLESKLSKQESVSHTLTAKKENVAPRDOEYD 461
      |||:||||| 1:||||: |||: ||| :|||:||||: ||| ||| :: 1:||||:
Db      122 KVGDDGYVFEENGYSRYIPAKNLSAETACIDSKLAKQESLSHKLGAAKTTDLPSSDREYRN 181

```

```

OY 462 KAYNLLTEAHKALFENKGRNSDFQALDKILLERLNDESTINKEKLVDDLLAFAPITHERL 521
    |||:| | : : |||| | :||| |||| | : : | ||||:||||| ||||
Db 182 KAYDLLARIHQDLLDNKGROVDFEALDNLIERLKVDSSDKKYLVDLLAFAPIRIHERL 241

```

[illegible]

**QY**

582	SDEKEVAAQAAYTTEKKGILPSPDADAVKANPTGDSAAAIYNRYVKGEKRIPLVRLPYMEHT	641
	: : :           :       :                 : : :           : : :	

**Db**

302	SEAEERAAAQAAYAKEKGLTPRSTPDHQSNTTEAKGAEAITYNRYKAACKVPPLDRMPYNIQYT	361
	:	

QY 642 VEKNGNLIIPKDHYNHKEFAWFDHYYKAPNGYTLLEDFATIKYYVEHPDERPSNDG 701  
|||||:||||| ||||||| |||: ||| ||||||| ||:|||||:|||||:|



Db 362 VEVKNGLSLIPHYDHYHNKKEFEWDEGLYEAPKGYTLLEDLLATVKKYYVEHPNERPHSDNG 421

QY 702 WGNASEHVLGKKDHSDEDPNKNFKADEEVEETPAEPEVPOVETEKEVEAOLKE 753  
:||||:| | : : | | :|||

Db 422 FGNASDHYXXNQPSQLSYSSASTSDNNTQSVAKGSTKPRANKSENLOSLKE 473

## RESULT 10

```

US-09-884-465A-376
; Sequence 376, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 376
; LENGTH: 999
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa = Methionine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (430)..(430)
; OTHER INFORMATION: Xaa = Glycine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (431)..(431)
; OTHER INFORMATION: Xaa = Proline or nothing
US-09-884-465A-376

```

Query Match	38.9%;	Score 1659;	DB 9;	Length 999;
Best Local Similarity	61.98;	Pred. No. 1.6e-96;		
Matches 326; Conservative	63;	Mismatches 98;	Indels 40;	Gaps 8;

QY	286	DIDSLKQLYKLP	LSQRHVESDGLVEDPQAITSRTARGVAVPHGDHYHFIPYSQMSELEE	345
Db	2	DIDSLKQLYKLP	LSQRHVESDGLIFDDPAQITSRRTARGVAVPHGNHNYHFIPYEQMSLEEK	61
QY	346	RIARIIPLRYRNSNHWP	DSRPQEOPSPQTPPEPSGPQPAPRNK-IDSN--SSLVSQLYR	401
Db	62	RIARIIPLRYSNHNWVP	DSRPEESPQTPPEPSSPQPAPNPQAPASNPIDEKLVEAVR	121
QY	402	KVGEGYVEEKGISRV	EFAKDLPSETVKNLESKLSKOESVSHLTAKENAVAPRDQEFYD	461
Db	122	KVGDBGYVEENGVSRYI	PAKNLSAETAAGIDSKLAKOESLSHKLGAKKTDLPPSDREFYN	181
QY	462	KAYNLLTEAHKALFENKGRNSDQALDKLLERLNDESTNKEKLVDDLAFAPLTRPERL	521	
Db	182	KAYDLLARIHQDLLDNKGRQVDFEALDNLRLERLKDVSSDKVLVDLIAFLAPTRHPERL	241	
QY	522	GKPNSQIEYTEDEVRIAQLADKYTTSDGYPFDEHDIISDEGDAYVTPHMGHSHTWGDSL	581	
Db	242	GKPNAGITTYTDEEIQVAKLAGKYTTEDGYIFDPRLDISDEGDAYVTPHMTHSHWIKKDSL	301	
QY	582	SDKEKVAOAQYTKKEGILPPSPDADAVKANPTGDSAAAIYNRVKGEKRIPLYRPLYMEHT	641	
Db	302	SEAERAAAOAYAKEKGLTPPSTDHQDSGNTAEAKGAEAIIYNRVKAACKVPLDRMPYNLOYT	361	
QY	642	VEVKNGNLIIPHKHDIHNIAFWFDHTTYKAPNGYTLLEDLFATIKYYVEHPDERPHSNDG	701	

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D0      362 VEVNGSLIIPHDYHNIKEFWEDEGLYEAPKGYTLLEDLLATVKYYVEHPNERPHSDNG   421

QY      702 WGNASEHVLGKDHSEDPNKNFKADEEPEVETPA-----EPVPQVETEKEVAEQ    750
       :|||:||| |::| ||:::||
D0      422 FGNASDHV--XXDLTEE--QIKAAQKHLEEVKTSHNGLDSLSSHEQDYF-----GN   468

QY      751 LKEAEVLLAKVTDDSLKANATEFTTLAGLRNNLTLOIMDNNSMAEAEK    797
       ||::||| |::| ::| ||
D0      469 AKEMKDLDKI-----EEKIAGIMKOYGVK--RESTIVNKER    503
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## RESULT 11

```

US-09-884-465A-377
; Sequence 377, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 377
; LENGTH: 999
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa = Methionine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (570)..(570)
; OTHER INFORMATION: Xaa = Glycine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (571)..(571)
; OTHER INFORMATION: Xaa = Proline or nothing
; US-09-884-465A-377

```

Query Match	38.7%	Score 1652;	DB 9;	Length 999;
Best Local Similarity	71.7%;	Pred. No. 4.4e-96;		
Matches 307; Conservative	50;	Mismatches 67;	Indels 4;	Gaps 2;

[illegible]

Db 872 SEAEERAAQAYAKEGLTPPSTHDODSGNTEAKGAELIYNRVKAAKAVPLDRMPYNLOYT 931  
QY 642 VEVKNGNLIIPKHDYHNKFAWEDDHTYKAPNGYTTLEDLFATIKYVEHPDERPHSNDG 701  
Db 932 VEVKNGSLIIPHYDHYHNKFEWDEGLYEA PKGYTTLEDLATV KYVEHPNERPHSDNG 991  
QY 702 WGNASEHV 709  
Db 992 FGNASDHY 999

RESULT 12  
US-09-884-465A-6  
; Sequence 6, Application US/09884465A  
; Publication No. US20030077293A1  
; GENERAL INFORMATION:  
; APPLICANT: Shire Biochem, Inc.  
; APPLICANT: Hamel, Josee  
; APPLICANT: Brodeur, Bernard  
; APPLICANT: Martin, Denis  
; APPLICANT: Charland, Nathalie  
; APPLICANT: Ouellet, Catherine  
; TITLE OF INVENTION: Streptococcus Antigens  
; FILE REFERENCE: 055190-0044  
; CURRENT APPLICATION NUMBER: US/09/884,465A  
; CURRENT FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: 60/212,683  
; PRIOR FILING DATE: 2000-06-20  
; NUMBER OF SEQ ID NOS: 384  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 1039  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-09-884-465A-6

Query Match 30.4%; Score 1295.5; DB 9; Length 1039;  
Best Local Similarity 41.5%; Pred. No. 1.5e-73;  
Matches 309; Conservative 99; Mismatches 185; Indels 151; Gaps 20;

QY 1 MKINKKYL-VGSAALILSVCSYELGLYQARTVKNRVSIDGKQATQKTENLTPDEVS 59  
Db 1 MKFSKKYIAAGSAVIVSLCLAYALNQHRSQENKDNRRVSYVDGSQSSQKSENLTDPDVS 60  
QY 60 KREGTNAEQIVIKITDQGYVTSBGDHYHYNGKVPYDAIISELLMKDPNYKLKDEDIVN 119  
Db 61 QKEGIAEQIVIKITDQGYVTSBGDHYHYNGKVPYDAIISELLMKDPNYQLKDADIVN 120  
QY 120 EVKGGYIVKVDGKYVYVYLKDAHADNVRTKEEINROKQEHSONREGTPRNDGAVALAR 179  
Db 121 EVKGGYIIVKVDGKYVYVYLKDAHADNVRTKEEINROKQEHVKDNE---KVNSNVAVAR 176  
QY 180 QGRYTTDDGYIFNASDIETDGYIVPHGDHYHYIPKNELSASELAAAEAFISGRNLS 239  
Db 177 QGRYTTNDGYVFNPAIDIEDTGNAVIVPHGHHYIPKSDLSASELAAAKAHLAKNMQP 236  
QY 240 NSRTYRONSNDNTSRTNMVPSVSNPGTTNTNTSNNSNTNSQASQSDIDSLKQLYKPL 299  
Db 237 SOLSYSTASDN-----NTQSVAKGSTSKPANKSENLOSLLKELYDSPS 280  
QY 300 SQRHVESDGLVFDPAQITSRITARGVAVPHGDHYHFIPYSOMSELEERARIIPLYRSNH 359  
Db 281 AQRYSSEGLVFDPAKISRTPNGVAIPHGDHYHFIPYSKLSALEEKIARMVP----- 333  
QY 360 WVPDSRPEQSPQPTPEPSPGPAPNLKIDSNSSLVSQLVKRVGEGYFEEKGISRYV 419  
Db 334 -----ISGTGSTVSTNAK----- 346  
QY 420 AKDLPEFYKNLESKLSQESVSHLTAKKENVAPRDQEFYDKAYNLLTEAHKALFENKG 479  
Db 347 -----PNEVYSSLSLSSNPSS-----LTSKELSSASDGYTFNPK-DIVEETATAYIVRHG 397  
QY 480 RNSDFQALDKLLERLNDESTNKEKLVDDLALFLAPITHPERLGKPNQIEYTEDEVRIAQ 539

Db 398 --DHFHYIPK-----SNQIGOPTLPNNSLATPSP-SLPINPGTSHEKHE----- 438  
QY 540 LADKYTSDGYTFDEHDIIISDEGDAYVTPHMGHSHWIGKDSLSDEKVAQAAYTKKJIL 599  
Db 439 -----EDGYGFEDANRIIAEDES GFVMSHGHDHNYFFKKDLTEEDIKAAQKHL 487  
QY 600 PPSPDADYKANPTG-DSSAAIYNRVK-----EKRIPLVRLPYMV--EHTVEV 644  
Db 488 -----VKTSHNGDLSLSSHEQDYPGNNAKEMKDLDKKIEKIAQIMQYGVKRESIVN 540  
QY 645 KNGNLIIPKHDYHNKFAWEDDHTYKAPNGYTTLEDLFATIKYVEHPDERPHSNDG-- 701  
Db 541 KEKNALITYPHGDHHDADP---IDEH---KPVGIG---HSHSNYELFRPEEGVAKKEG 590  
QY 702 --WGNASEHVLGKKDHSEDPKNKF 723  
Db 591 VYTGEELTNVNLKNSTFNNQNF 614

RESULT 13  
US-09-765-272-182  
; Sequence 182, Application US/09765272  
; Patent No. US20020061545A1  
; GENERAL INFORMATION:  
; APPLICANT: Choi et. al.  
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
; NUMBER OF SEQUENCES: 452  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/765,272  
; FILING DATE: 22-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/961,083  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB340P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 182:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 447 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 182:  
US-09-765-272-182

Query Match 27.8%; Score 1186.5; DB 10; Length 447;  
Best Local Similarity 41.0%; Pred. No. 3.5e-67;  
Matches 263; Conservative 62; Mismatches 110; Indels 207; Gaps 11;

QY 24 LGLYQARTVKNRVSIDGKQATQKTENLTPDEVSKREGINAEOIVIKITDQGYVTSHG 83  
Db 1 LNQHRSQENKDNRRVSYVDGSQSSQKSENLTDPDVSQKEGIAEQIVIKITDQGYVTSHG 60  
QY 84 DHYHYNGKVPYDAIISELLMKDPNYKLKDEDIVNEVKGGYVIVKVDGKYVYVYLKDAHA 143

```

Db      61 DHYHYNGKVPYDALFSEELMLKDPNYQLKDADIVNEVKGGYITIKVDGKYVYLKDAANA 120
QY      144 DNVRTKEEINROKOEHSQHREGGTPRNDGAVALARSGRYYTDDGYIFNASDIIEDTGDA 203
Db      121 DNVRTKDEINROKQEHVKDNE-----KNSNVAVARSQGRYTTNDGYVFNPAIDIETGNA 176
QY      204 YIVPHGDHYHYIPKNELSASELAANAFAFLSGRGNLSNRYTRRONSNDNTSRTNWPVSVSN 263
Db      177 YIVPHGCHYHYIPKSDLSASELAAKAHLAGKNMOPSQLSYSSSTASDN----- 224
QY      264 PGTTNTNTSNNSTNSQASQSDNDIDSLKQLYKLPLSQRHVESDGLVDPQAQTSRTARG 323
Db      225 -----NTQSVAKSGSTSKPANKSENQSLKELYSQAQRYSESDGLVDFPAKIISTRPNG 280
QY      324 VAVPHGDHYHFIPYSQMSLEERIARIPLRYRSNHWVPDSRPEQSPQPTPEPSPGPQP 383
Db      281 VAIIPHGDHYHFIPYSKLSALEEKIARMVP----- 309
QY      384 APNLKIDNSSSLVSQLVKRVGEGVFEKGISRYVFAKDLPSETVKNLESKLSKQESVSH 443
Db      310 -----ISGTGSTVSTNAK-----PNEVVSSLGSLSSNPSS--- 339
QY      444 TLTAKKENVAPRDOEFYDKAYNLLTEAHKALFENKGRNSDFQALDKLLERLNDESTNKEK 503
Db      340 -LITSKE-----LSSA----- 349
QY      504 LVDDLALFLAPITHPERLGPNSOIEYTEDEVRIAQLADKYTTSQGYIFDEHDIISDEGD 563
Db      350 -----SDGYIFNPKDLYEETAT 366
QY      564 AYVTPHMGSHWIGKDSLDSKEVAAQAAYTKERGIPLPSPDADYKANP-----TGDSA 616
Db      367 AYIVRHGDHFHYI-----PKSNOIGQPTLPNNSLATPSPSLPI--NPGTSHEKHEEDGY 418
QY      617 AAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGLIIPHKDHYH 658
Db      419 GFDANRIAE-----DESGFVMSHGHDHNH 442

RESULT 14
US-09-884-465A-384
: Sequence 384, Application US/09884465A
: Publication No. US20030077293A1
: GENERAL INFORMATION:
:   APPLICANT: Shire Biochem, Inc.
:   APPLICANT: Hamel, Josee
:   APPLICANT: Brodeur, Bernard
:   APPLICANT: Martin, Denis
:   APPLICANT: Charland, Nathalie
:   APPLICANT: Ouellet, Catherine
:   TITLE OF INVENTION: Streptococcus Antigens
:   FILE REFERENCE: 055190-0044
:   CURRENT APPLICATION NUMBER: US/09/884,465A
:   CURRENT FILING DATE: 2001-06-20
:   PRIOR APPLICATION NUMBER: 60/212,683
:   PRIOR FILING DATE: 2000-06-20
:   NUMBER OF SEQ ID NOS: 384
:   SOFTWARE: PatentIn version 3.1
:   SEQ ID NO 384
:   LENGTH: 913
:   TYPE: PRT
:   ORGANISM: Artificial Sequence
:   FEATURE:
:   OTHER INFORMATION: Unknown Organism
:   NAME/KEY: MISC_FEATURE
:   LOCATION: (1)..(1)
:   OTHER INFORMATION: Xaa = Methionine or nothing
:   NAME/KEY: MISC_FEATURE
:   LOCATION: (344)..(344)
:   OTHER INFORMATION: Xaa = Glycine or nothing
:   NAME/KEY: MISC_FEATURE
:   LOCATION: (345)..(345)

```

OTHER INFORMATION: Xaa = Proline or nothing  
US-09-884-465A-384

Query Match	23.2%;	Score 991.5;	DB 9;	Length 913;
Best Local Similarity	55.4%;	Pred. No. 2e-54;		
Matches 189;	Conservative 45;	Mismatches 70;	Indels 37;	Gaps 22;

QY	507	DLLAFLAPITHBERLGKPNŠQIEVTEDEVRIAQLADKYTTSDGYTFDEHDIISDEGDAYV	566
		:                             :     :   :   :	
Db	2	DILAFLAPIRHPERLGKPNŠQIITVTEDEIQVAKLAGKYTTEDEGYTFDPDRIITSDEGDAYV	61
QY	567	TPHMGHSHWIGKDSLSDKEKVAAQAYATEKGILLPPSPDADVKANPTGDSAAAIYNRVKGE	626
		:	
Db	62	TPHMTSHHWIKKDSLSEVERAAQAYAKEKGLTPPSTDHQSQNTAEKAGAEAIYNRVKAA	121
QY	627	KRIPLVRLPYWVEHTVEVKGNGNLIFPKDHYHNIKFAWFEDDHTYKAPNGYTTLEDLFATIK	686
		: :           : :	
Db	122	KKVPLDRMPYNLQYTVVEVKGNSLIIFHYDHYHNIKFEWFEDGLYEAPKGYSLLEDLLATYK	181
QY	687	YVVEHPDERPHSNDGWNASEHYLGK-----KDHSE-----	717
		:	
Db	182	YVVEHPNERPHSDNGFGNASDHYRKNKADQDSKPDDEKHEDEVSEPTHPESDEKENHAGL	241
QY	718	-----DPNKNFKADEEPVEETPPAPEVPQVETEKVEAQLEAEVLLAKVTDSSLRAN	769
		: : :   :                               :   : :	
Db	242	NPSADNLTKPSTDTEETEETEEAEEDTIDEAEIPIQVENSVINAKIADADEALLEKVTDPSTIRON	301
QY	770	ATEITLAGLRNNLTLQIMDNNSIMAEKLLALLKGSNPSSV	810
		: :	
Db	302	AMEITLTGLKSSLLGTCKDNNTISAEVDSLALLKESQAPIT	342

RESULT 15  
US-09-884-465A-379

```

; Sequence 379, Application US/09884465A
; Publication No. US20030077293A1

```

APPLICANT: Shire Biochem, Inc.  
 APPLICANT: Hamel, Josee  
 APPLICANT: Brodeur, Bernard  
 APPLICANT: Martin, Denis  
 APPLICANT: Charland, Nathalie  
 APPLICANT: Ouellet, Catherine  
 TITLE OF INVENTION: Streptococcus Antigens  
 FILE REFERENCE: 055190-0044  
 CURRENT APPLICATION NUMBER: US/09/884,465A  
 CURRENT FILING DATE: 2001-06-20  
 PRIOR APPLICATION NUMBER: 60/212,683  
 PRIOR FILING DATE: 2000-06-20  
 NUMBER OF SEQ ID NOS: 384  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 379

```

; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa = Methionine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (344)..(344)
; OTHER INFORMATION: Xaa = Glycine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (345)..(345)
; OTHER INFORMATION: Xaa = Proline or nothing
US-09-884-465A-379

```

Query Match	23.2%;	Score 991.5;	DB 9;	Length 1152;
Best Local Similarity	55.4%;	Pred. No. 2.8e-54;		
Matches 189;	Conservative 45;	Mismatches 70;	Indels 37;	Gaps 2;
507	DLAFLAPITHTPERLCKPN	SOIEYTEDEVR	IAQLADKYTTSDG	IFDEHDIISDEGDAYV 566

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Db      2  DILAFIAPIRHBERLGKPNAOITYTDEIQVAKLAGKYTTEGCIYFDPRDITSDEGDAYV 61
QY      567 TPHMGSHWIGKDSLSDEKVAQAQYTKKGIILPSPDADAVKANPTGDSAAAIYNRVKG 626
Db      62  TPHMTHSHWIKDLSSEAERAAQAQYAKKGLTPSTDHQDSGNTAKGAELIYNRVAKA 121
QY      627 KRIPLVRLPYMVEHTEVEVKNGLIIPKDHVHNKIFAWFDDHTYKAPNGYTLLEDLFAPIK 686
Db      122 KKVPLDRMPYNIQYTVVEVKNGLIIPHYDHYHNKIFEFWFDEGLYEAPKGYSLLEDLATYK 181
QY      687 YVEHPDERPHSNDGNGNASEHVLGK-----KDHSE----- 717
Db      182 YVEHPNERPHSDNGGNGNADHVRKKNKADQDSKPDEDEKHEDEVSEPTHPESDEKENHAGL 241
QY      718 -----DPNKNPKADEEPVEETPAPEVPQVETEKVEAQLKEAEVLLAKVTDSSLKAN 769
Db      242 NPSADNLKPPSTDEETEEDTDEAEIPOVENSVINAKIADAEALLESKVTDPSTRON 301
QY      770 ATETLAGLRNNLTQIMDNNSIMAEAEKLLALLKGSNPSSV 810
Db      302 AMETLTGLKSSLLGTTKDNNTISAEVDSLALLKESQAPAPI 342
```

Search completed: May 19, 2003, 08:24:12  
Job time : 242.436 secs